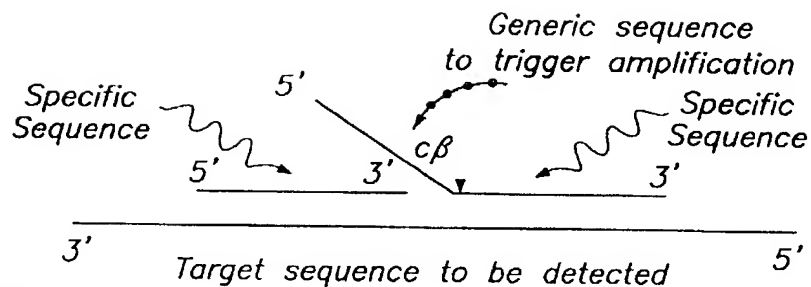
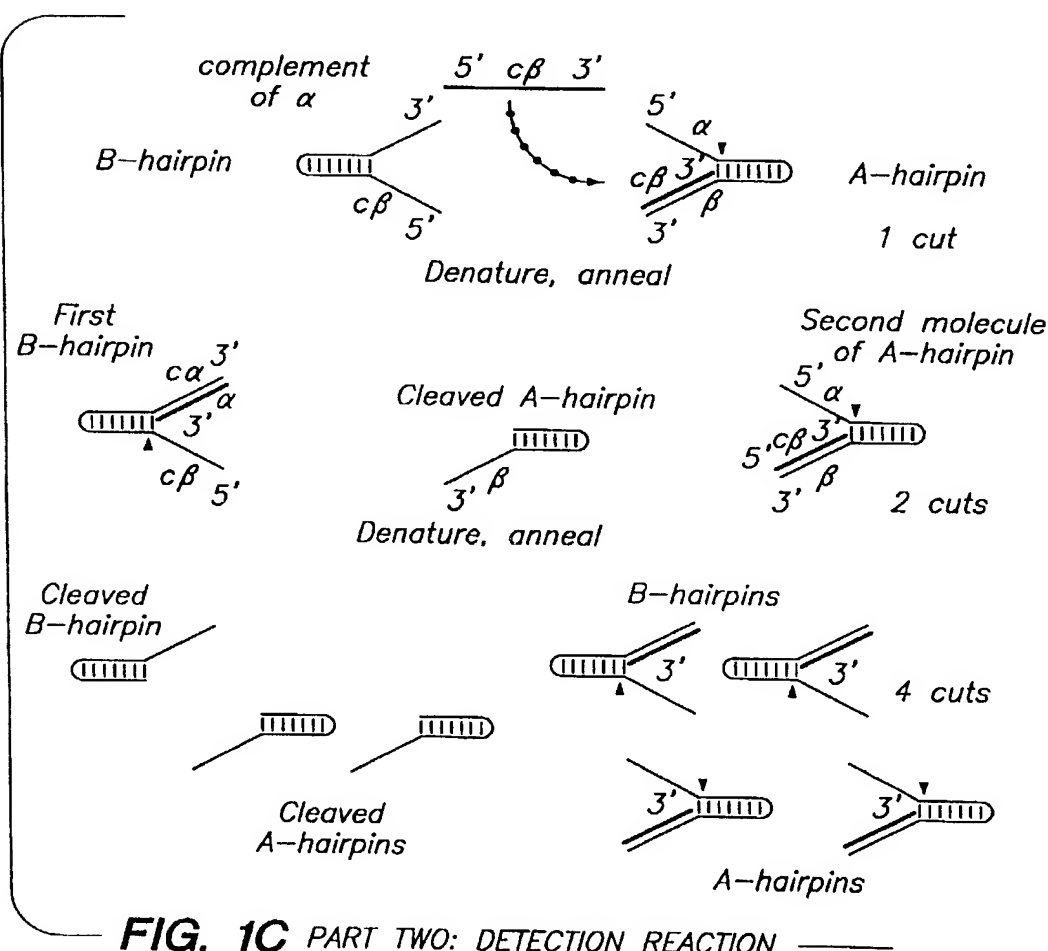


FIG. 1A



**FIG. 1B** PART ONE: TRIGGER REACTION



**FIG. 1C** PART TWO: DETECTION REACTION



FIG. 2B

MAJORITY [SEQ ID NO:73] CGAGCGCGGACGACGCTXCTGGCCACCCCTGGCCCAAGAACGGCGAAAGGAGGGGTACGAGGTGGGCATCCTC

DNAPTAQ [SEQ ID NO:1] .....C.....G.....C.....C..... 417  
 DNAPTFL [SEQ ID NO:2] T.....G.....CG..... 414  
 DNAPTTH [SEQ ID NO:3] .....T..C..... 420

MAJORITY ACAGCGGACCGCGACCTCTACGAGCTCCTTCGGACCGCATCGCCGTCCTCCACCGGAGGGGTACCTCA

DNAPTAQ .....AAA.....T.....CA..... 487  
 DNAPTFL ..T.....G..G.....A.....T.....G.. 484  
 DNAPTTH .....A..G.C.....G.....CC..... 490

MAJORITY TCACCGCGCGGCTGGCTTGGGAGAACTACGCCCTGAGGCCCGGAGCACTGGGTGGACTACCGGGCCCTGGC

DNAPTAQ .....C.....A.....C..C.....CC.....A.. 557  
 DNAPTFL .....AC.....C.C..... 554  
 DNAPTTH .....A.....C.....T..C.....C.T 560

MAJORITY GGGGACCCCTCGGACAAACCTCCCGGGGTCAAGGGCATCGGGGAGAAAGACCGCCCGGAGGCTGCTCXAG

DNAPTAQ C.....GAG.....T.....G..GAG.....T..GG.. 627  
 DNAPTFL .....G..T..A.....G.....A..G.....A..GGC.. 624  
 DNAPTTH .....A.....T.....TC.....A... 630

MAJORITY GAGTGGGGGAGCGCTGGAAAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC...CXTCCGGGGAGAGA

DNAPTAQ .....GC.....A..... 694  
 DNAPTFL .....T..C..C.....A.....T.....T..G.....C 691  
 DNAPTTH .....A.....A.....A.AAA..G..... 700

**FIG. 2C**

MAJORITY [SEQ ID NO:7]	TCCAGGCCACATGGAXGACCTGAXGCTCTCCTGGAGCTXTCCAGAGTGGGACCGACCTGCCCCCTGGA	
DNAPTAO [SEQ ID NO:1]	.....T.....C..T...A.....C..GG..A.....	764
DNAPTEL [SEQ ID NO:2]	.....GGG.....G..C....GCC..T...C..A...T.....A...T.....	761
DNAPTTH [SEQ ID NO:3]	.....A.....C.....C.....C..G.....T.....C...G.....C.....	770
MAJORITY	GGTGGACTTCGCCAAGXGGCGGGAGCGCGGACCGGAGGGGCTTAGGGCCCTTCTGGAGAGCGCTGGAGTTT	
DNAPTAO	.....AA.....A.....A.....	834
DNAPTEL	.....GG..G..C..C..CACA...A...T.....T..GG...T...T.....C..T.....	831
DNAPTTH	.....C.....C...G.....	840
MAJORITY	GGCAGGCTCCTCCACGAGTTCGGGCTCCTGGAGGGCGCCCAAGGCCCTGGAGGAGGCCCCCTGGCCCGCCCG	
DNAPTAO	.....T.....AA.....	904
DNAPTEL	.....A.....G.....G..G....GGCA.....	901
DNAPTTH	.....C.....GCCC.....	910
MAJORITY	GGCAAGGGGCGCTTCCTGGGCTTGTCCCTTCCCGCCCCGAGCCCATGTGGCGCGAGCTTCTGGCCCTGGC	
DNAPTAO	.....G.....AAG.....T.....	974
DNAPTEL	.....T..TT.....TC.T.....T.....	971
DNAPTTH	.....C.....C.....G.....AAA.....	980
MAJORITY	CGCGCGCAGGGAGGGCGGCTCCACCGGGGACGACGCCCTTTAXGGGCGCTXAGGGACCTXAAGGAGGTG	
DNAPTAO	.....G.....C..C..G..T..A..AA..C...C.....G.....C.....	1044
DNAPTEL	T..GG..GT.....G..CC...T.....A.....C...G.....G.....T....G....	1041
DNAPTTH	.....TG.....C.....G.....GGC...G..A..A.....C.....C.....C.....	1050

FIG. 2D

MAJORITY [SEQ ID NO:7] CCGGGGXCCTGCTGGCCAGGACCTGGCCGTTTGGCCCTGAGGGAGGGCCCTXGAGCCTCTGCCCCGGGGAGCG

DNAPTAQ [SEQ ID NO:1] .....G..T.....A.....AG....C.....A.....T.G....CC.....C.... 1114

DNAPTFL [SEQ ID NO:2] .....AA....G.....G.....C.....G.....T.C..A.A..... 1111

DNAPTTH [SEQ ID NO:3] .....C.....C.....C.....TC.....G.A.....G..... 1120

MAJORITY ACCCGCATGCTGCTGGCCTACCTGCTGGACCCCTGCAACACACCCCGGAGGGGGTGGCCCGGGCGCTACGG

DNAPTAQ .....T.....T..... 1184

DNAPTFL .....G.....T.....T..... 1181

DNAPTTH .....T.....G..... 1190

MAJORITY GGGGGAGTGGACGGAGGAXCGGGGGGAGCGCCGCTCTGCGGAGGGCTCTTCCXGAACCTXXGGAG

DNAPTAQ C.....G.....G.....T.....GCC.....GTG..G. 1254

DNAPTFL .....T.....A.....GG.....C.G.....A..C...AAA.... 1251

DNAPTTH .....C..C.CCC.C.....C..G.....CAT.G.....CCTTA.. 1260

MAJORITY CCGCCTTGAGGGGAGGAGAGGCTCCTTTGGCTTTACGAGGAGGTGGAGAGCCGCTTCCCGGGTCCCTGG

DNAPTAQ A.G.....G.....G.....G.....GCT..... 1324

DNAPTFL .....A....A..A.AC.C..G.....G.....G.....GT... 1321

DNAPTTH .....C.....A.....C.....C.....A.....G..... 1330

MAJORITY CCCACATGGAGGCCACGGGGGTXCGGCTGGAGCTGGGCTACCTCCAGGGCCCTXTCCTGGAGGTGGCGGA

DNAPTAQ .....G..C.....C.....T..AG....T.G.....C.. 1394

DNAPTFL .....GG.....C.....C.....C.....A..C 1391

DNAPTTH .....C.....C.....A.....T.....T.....C.T..... 1400

FIG. 2E

MAJORITY [SEQ ID NO:7]	GGAGATCGGGCGGCTCGAGGAGGAGGCTTTCCGGCCTGGCGGGGCGACGGCTTCAACCTCAACTCCCGGGGAC	
DNAPTAQ [SEQ ID NO:1]	.....GC.....CC.....	1464
DNAPTFL [SEQ ID NO:2]	.....G.C....AG..G.....	1461
DNAPTTH [SEQ ID NO:3]	.....T.....G.....	1470
MAJORITY	CAGCTGGAAGGCTGCTCTTTGACGAGGCTXGGGGCTTCCCGGCCATCGGCAAGAGCGGAGAGACXGGGCAAGC	
DNAPTAQ	.....C.....A.....C.....	1534
DNAPTFL	.....GC.....G.C..G..T.....	1531
DNAPTTH	.....TA.....T.G..G.....	1540
MAJORITY	GCTCCAGCAGCGCGCGCGCTGCTGGAGCGCGCTXCGXGAGGGCGCCACGGCCATCGTGGAGAGAGATCCTGCAGTA	
DNAPTAQ	.....C.....C..C.....	1604
DNAPTFL	.....T.....G..A.....CGGC.....	1601
DNAPTTH	.....G.....A..G.....C...C..	1610
MAJORITY	CCGGGAGGCTCACCAGGCTCAAGAAACAGCTACATXGACCGCGCTGCCXGXGCTCGTCCACGCCAGGACGGGC	
DNAPTAQ	.....G...G.....T.....T....G.A....A.....	1674
DNAPTFL	.....A.....C.C...G.....A...C...C...	1671
DNAPTTH	.....G.G.....G..AAG.....G.....	1680
MAJORITY	CGGCTCCACACCGCGCTTCAACGAGACGGCGCAGCGGCGCAGGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAQ	.....A.....A.....T.....C..	1744
DNAPTFL	.....G.....C.....TCC.....	1741
DNAPTTH	.....G.....G.....	1750

FIG. 2F

MAJORITY [SEQ ID NO:7]	AGAACATCCCGTCCGACCCGCTGGGCGAGGATCCGCCGGCCTTCGTGGCCGAGGGGTGGGT	
DNAPTAQ [SEQ ID NO:1]	.....G..T..G.....A.C.....G...C.	1814
DNAPTFL [SEQ ID NO:2]	.....G.....T.....C.C.....A.....C.....	1811
DNAPTTH [SEQ ID NO:3]	.....CT.....C.....C...T...G	1820
MAJORITY	GTTCGTGGCCCTGACTATAGCCACATAGAGCTCCGGTCTTCGCCCACTCTCCGGGACGAGAACCTG	
DNAPTAQ	A.....A.....G.....C.....	1884
DNAPTFL	.C.....T.T.....C.....T.....	1881
DNAPTTH	.....C.....C.....C.....A.....	1890
MAJORITY	ATCCGGTCTTCCAGAGGGGAGGACATCCACACCCAGAGCCGCGCTGGATGTTCGGCTCCGCCCGG	
DNAPTAQ	.....C.....GG.....G...G..	1954
DNAPTFL	.....T.....T.....TT...G.	1951
DNAPTTH	...A.....A.....A.....	1960
MAJORITY	AGCCGTGGACCCCTGATGCCCGCGGGCCAGACCATCAAGTGGGGTCTCTACGGCATGTCCGC	
DNAPTAQ	.....G...G...G...G...G...G...	2024
DNAPTFL	.A.GG..A...T.....G.....	2021
DNAPTTH	.....GG.G.....G.....	2030
MAJORITY	CCACCGCTCTCCAGGAGCTTCCCATCCGTAGGAGGGGGTGGCTTATTGAGCGCTACTTCCAG	
DNAPTAQ	.....A.....T.....CCA.....T...	2094
DNAPTFL	.....GG.....T.....	2091
DNAPTTH	...TA.G.....T...A.....A	2100



FIG. 2G

MAJORITY [SEQ ID NO:7]	AGCTTCCCAAGCTGGGGGCTGGATTGAGAAAGCCCTGGAGGAGGGCAGAGGGGGGTACGTGGAGA	2164
DNAPTAQ [SEQ ID NO:1]	.....	2161
DNAPTFL [SEQ ID NO:2]	....A.....GG.....C.....C.CC.....T.....	2170
DNAPTTH [SEQ ID NO:3]	.....A..A.....G...A.....C.....A..	
MAJORITY	CCCTCTTGGGGCGGGGGCTAGCTGCCCGACCTCAACGGCGGGGTGAAGAGCGTCCGGCAGCGGGCGGA	
DNAPTAQ	.....C.....A.....AG.C.....C..	2234
DNAPTFL	.....T.....	2231
DNAPTTH	.....AA.AA.....CA.....C.....	2240
MAJORITY	GGGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCGCGGACCTCATGAAGCTGGCCATGGTGAAGCTC	
DNAPTAQ	.....	2304
DNAPTFL	.....G.....T.....	2301
DNAPTTH	.....C.....	2310
MAJORITY	TTCGCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCACGACGAGCTGCTCCTCGAGGGCCC	
DNAPTAQ	.....A....GG.....T.....	2374
DNAPTFL	.....T.....C.....G.....TT.G.....G.....	2371
DNAPTTH	.....C..C.G..G.....C.C.....C.....CC.....G.....	2380
MAJORITY	CCAAAGAGGGGGGAGGXGGTGGCCGCTTGGCCCAAGAGGTCATGGAGGGGCTCTATCCCTCGGCGGT	
DNAPTAQ	.A.....A.....CC.....CGGC.....G.....	2444
DNAPTFL	....G..C.....AG...A.....GG.....CAG..	2441
DNAPTTH	..C...C.....C....A.....G.....C.....AA..C.....C.....	2450

FIG. 2H

MAJORITY [SEQ ID NO:7]	GGCCCTGGAGGCTGGAGGCTGGGGATGGGGGAGGACTGGCTCTCGGCCAAGGAGTAG
DNAPTAQ [SEQ ID NO:1]	.....A.....GA
DNAPTFL [SEQ ID NO:2]	.....CC.....
DNAPTTH [SEQ ID NO:3]	.....T.....GT...

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FIG. 3A

MAJORITY [SEQ ID NO: 8]	MXAMLPLEFPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPUQAVYGFAXSLLKALKEDG-DAVXVVFDKAK	
TAQ PRO [SEQ ID NO: 4]	RG.....H.....I.....	69
TFL PRO [SEQ ID NO: 5]	.....V.V.....	68
TTH PRO [SEQ ID NO: 6]	.....YK..F.....	70
MAJORITY	APSFRAHEAYKACRAPTPEDFPROLALIKELVDLLGLXRLEVPQYEADDDVLATLAKKAEKEGYEVRI L	
TAQ PRO	GG.....A.....S.....	139
TFL PRO	.....V.....F.....R.....	138
TTH PRO	.....FT.....	140
MAJORITY	TAORDLYQLLSDRI AVLHPGEGYLITPAWLWEKYGLRPEQWVDYRALXGDPDSNLPQVKGI GEKTAXKLLX	
TAQ PRO	K.....H.....D..A.....T..E.....R...E 209	
TFL PRO	E...I.....Y.....A.....I.....GR..IR 208	
TTH PRO	V...V.....H...E.....F...V.....L...K 210	
MAJORITY	EWGSLNLLKNLDRVKP-XXREKIXAHMEDLXLSSXLSXVRTOLPLEVDFAFXRREPDREGLRAFLERLF	
TAQ PRO	A.....L...AI...L...D..K..WD.AK.....K.....R.....	278
TFL PRO	FQH...O...SL...IQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTH PRO	ENV...K..L...R..LE..R.....L.OG.....	280
MAJORITY	GSLLHEFGLLXPKALEEAPWPPPEGAFVGVLSRPEPMWAE LLALAAAXGRVHRAXDPLXGLRDIKEV	
TAQ PRO	S.....K.....D.....G.....PE.YKA.....A 348	
TFL PRO	G...A.....L.SF.....G.WE..L...Q...R.....G. 347	
TTH PRO	A.AP.....K.....C.D.....A...A...K..... 350	

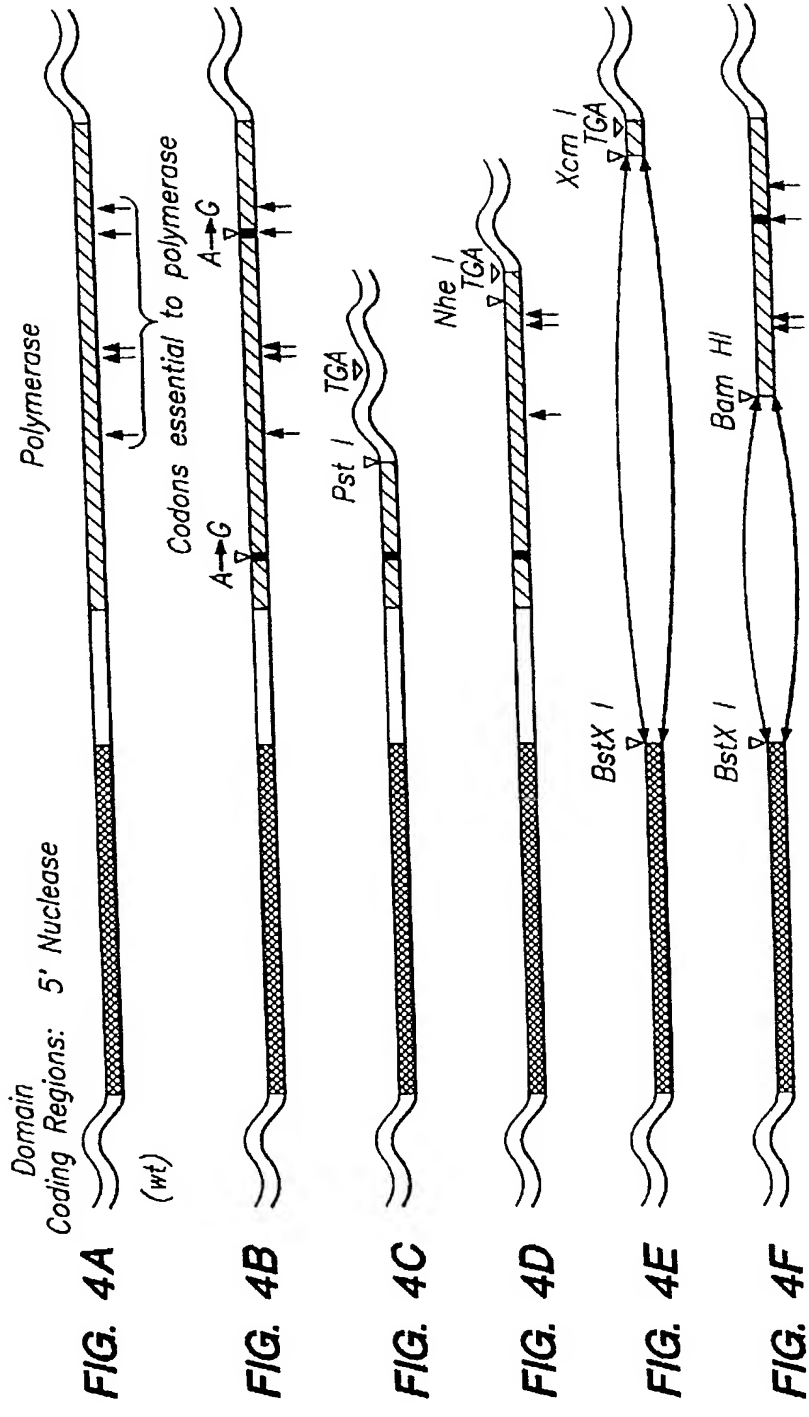
FIG. 3B

MAJORITY [SEQ ID NO: 8]	RGLLAKOLAVLALREGDLXPDDPMLLAYLLDPSNTTPEGVARRYGGENTEDAGERALLSERLFXNLXX	
TAQ PRO [SEQ ID NO: 4]	S.....G.P.....E.....A.....A.....WG	418
TFL PRO [SEQ ID NO: 5]	I.....F.E.....A.....QT.KE	417
TTH PRO [SEQ ID NO: 6]	S.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLSEEVFRLAGHPFNLNSRD	
TAQ PRO	R...R...A.....R.....A...A.....	488
TFL PRO	K...E.....R.....EA.V.O.....	487
TTH PRO	K...H.....L.....	490
MAJORITY	OLERVLFDELGLPAIGKTEKTKRSTSAVLEALREAHPIVEKILQYREITKLKNTYIDPLPXLVHPRTG	
TAQ PRO	.....S.....D.I.....	558
TFL PRO	.....DR.....A...K..	557
TTH PRO	R...L...Q.....H.....V...S.....	560
MAJORITY	RLHTRFNOTATATGRLSSSDPNLQNI PURTPIGQRI RRAFVAEEGWXLVALDYSOIELRVLAHLSCDENL	
TAQ PRO	.....I.....L.....	628
TFL PRO	.....V..V.....	627
TTH PRO	.....A..A.....	630
MAJORITY	IRVFQEGRDIHTQTASWMFGVPPPEAVDPLMRRRAKTI NFGVLYGMSAHLRSOELAI PYEEAVAFI ERYFQ	
TAQ PRO	E.....R.....Q.....	698
TFL PRO	S..G.....G..S.....	697
TTH PRO	K.....V.....	700

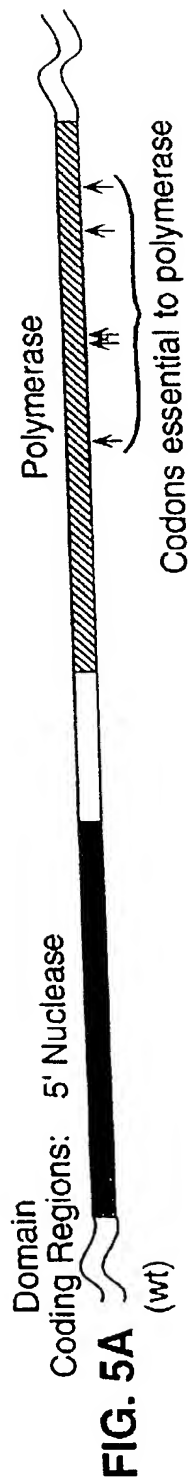
FIG. 3C

MAJORITY	[SEQ ID NO: 8]	SFPKVRAWI EKTLEGGRRRGYVETLFCRRRYVPDLNARVKSUREAERMAFNMPVQGTAAADLMKLAHVKL	768
TAQ PRO	[SEQ ID NO: 4]	.....E.....	767
TFL PRO	[SEQ ID NO: 5]	Y.....G.....R.	770
TTA PRO	[SEQ ID NO: 6]	.....K.....	
MAJORITY FPRLXEMGARM LLOVHDELVLLEAPKXRAEXVAALAKEVME GUYPLAVPLEVEVGXGEDWLSAKEX			
TAQ PRO	.....E.....E...A...R.....I.....	833	
TFL PRO	.....O.L.....D...R.....W.O.....L.....	831	
TTA PRO	.....R.....L...QA...E.....A..KA.....M.....G	835	

Genes for Wild-Type and Pol(-)DNAP<sub>Taq</sub>



# Genes for Wild-Type and Pol(-) DNAPTfl



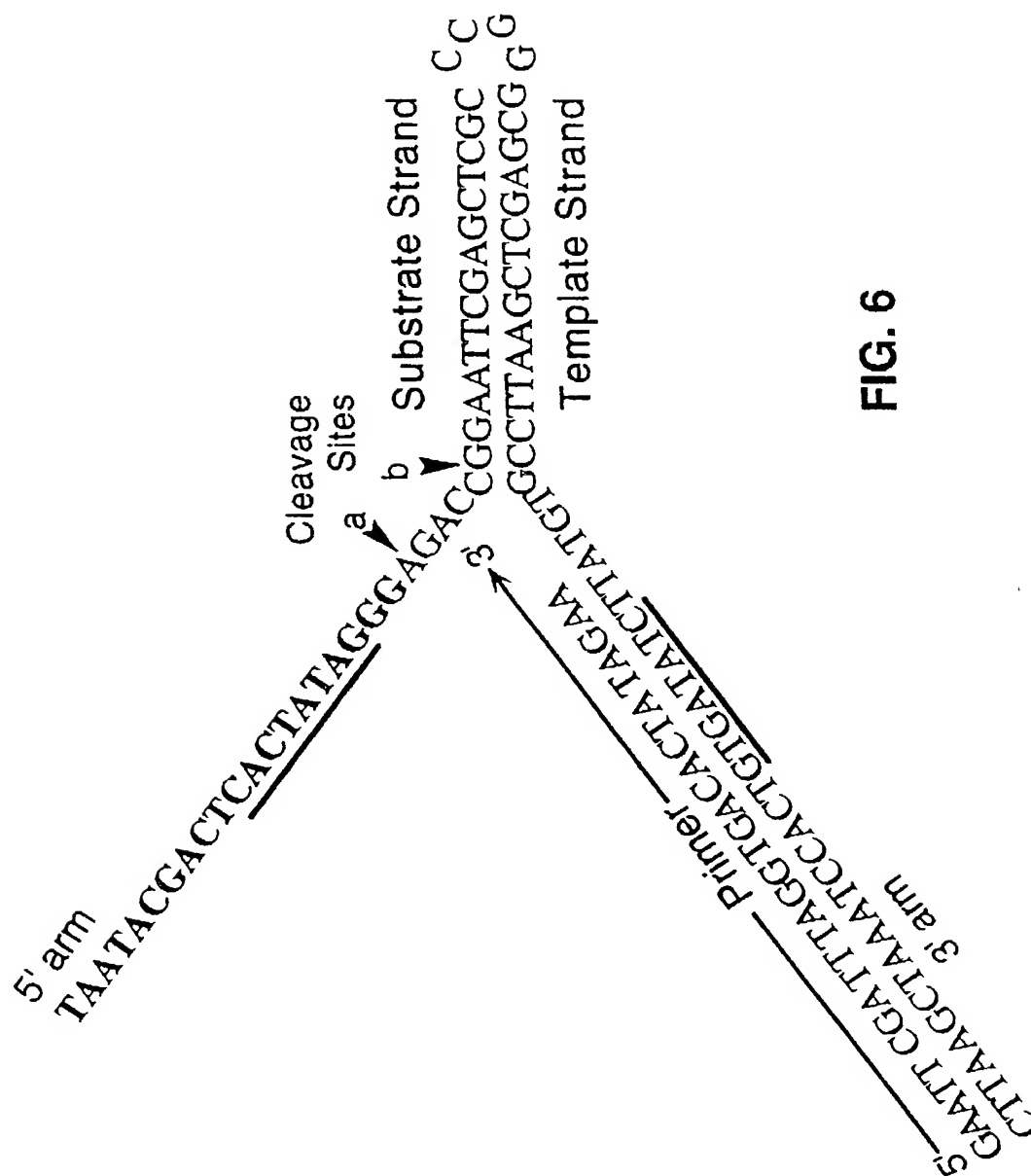
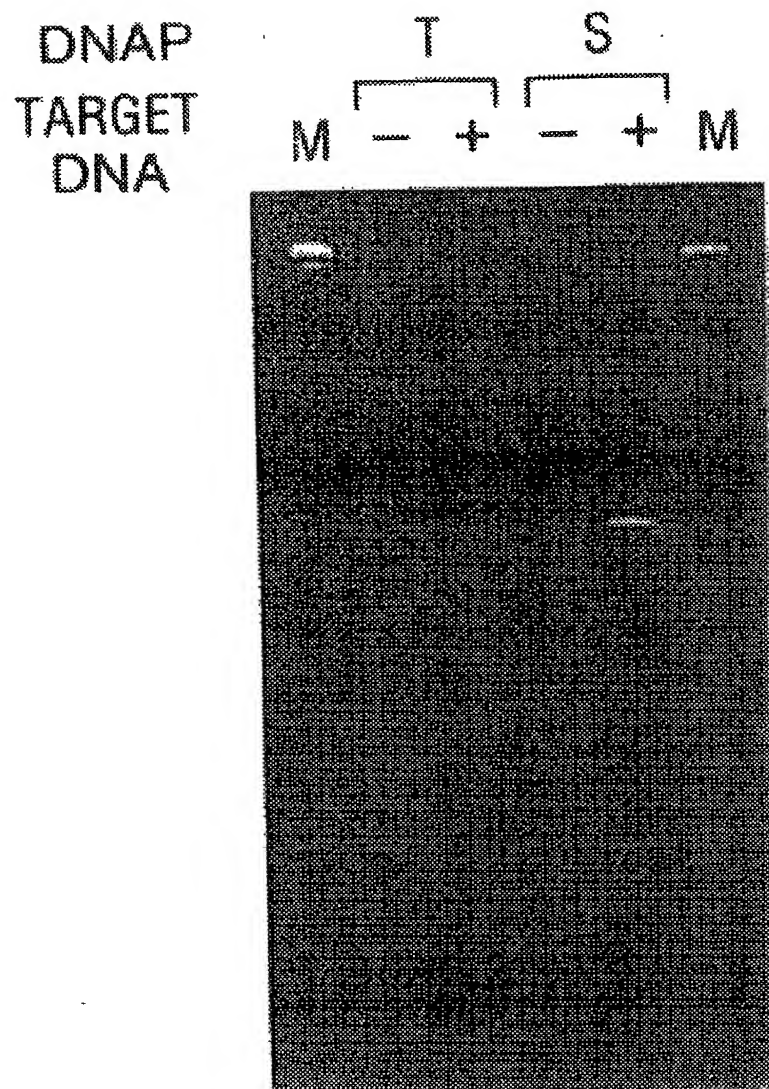
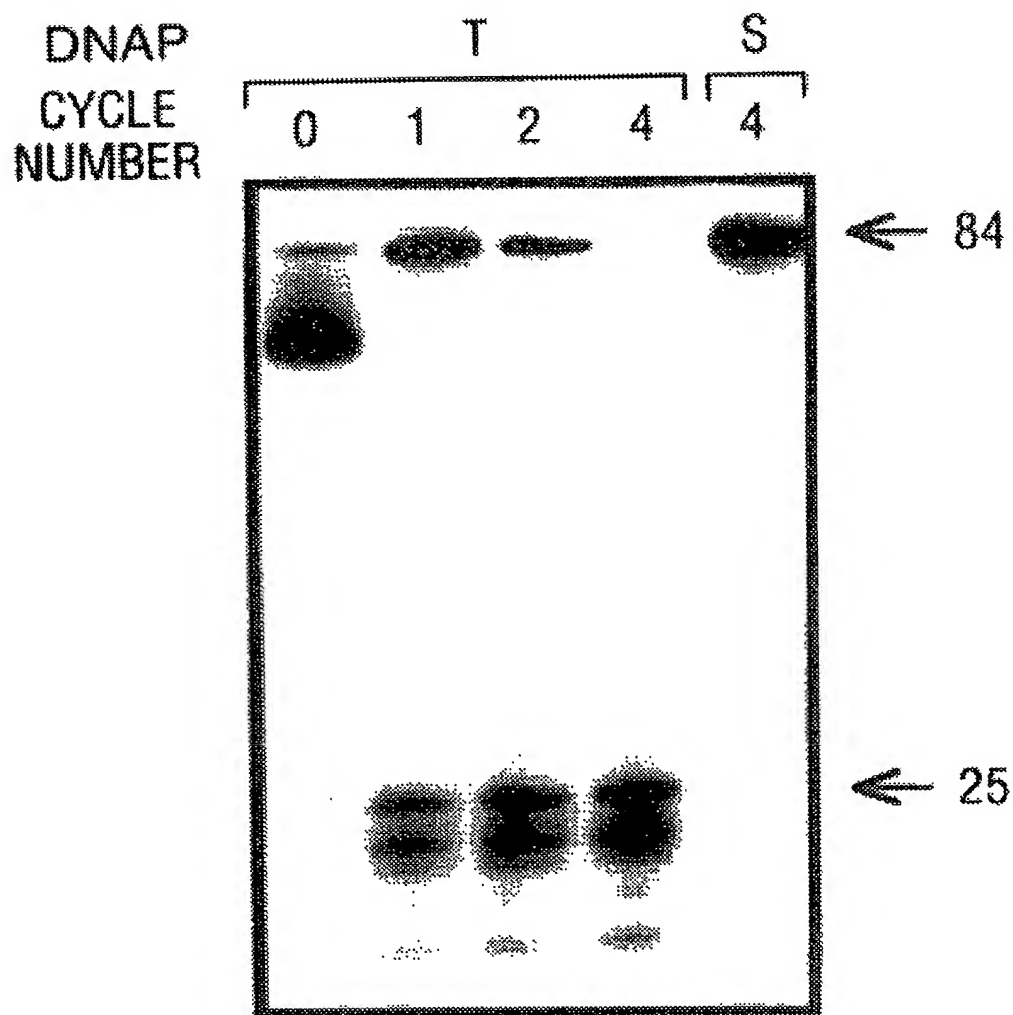


FIG. 6



**FIG. 7**

**FIG. 8**

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

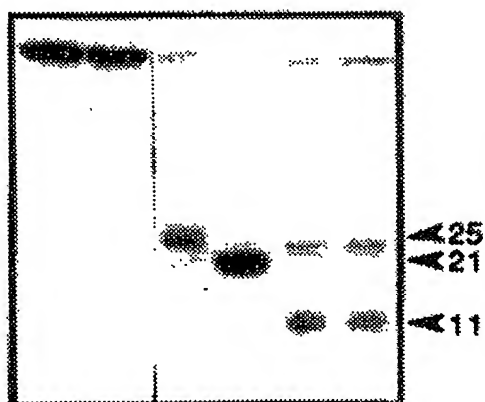
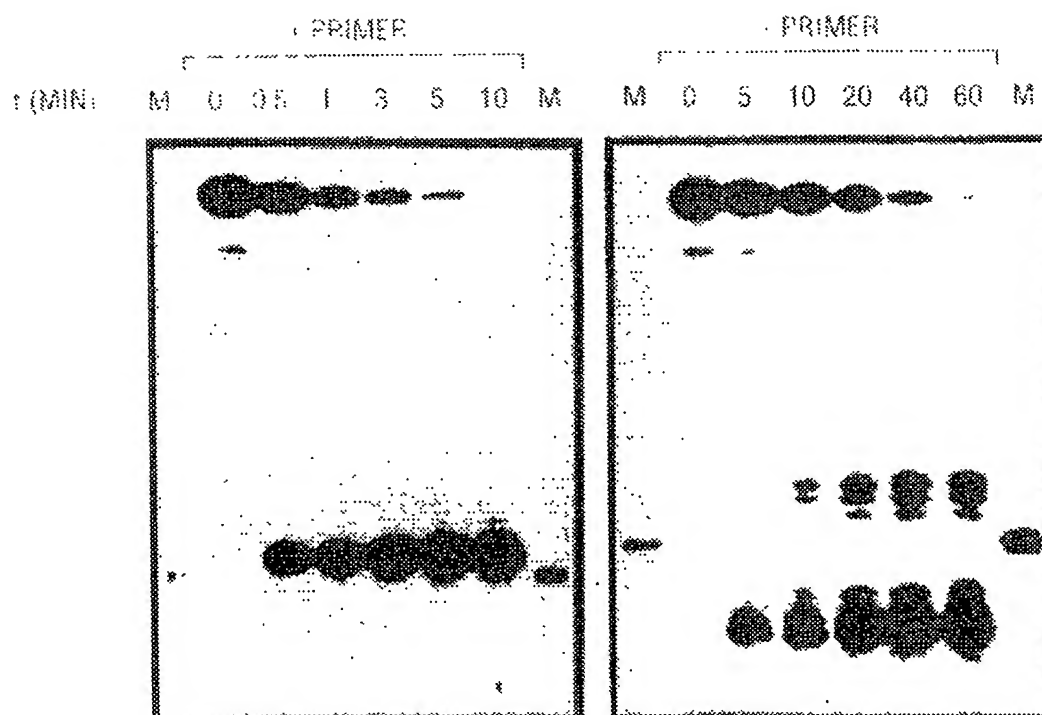


FIG. 9A



FIG. 9B



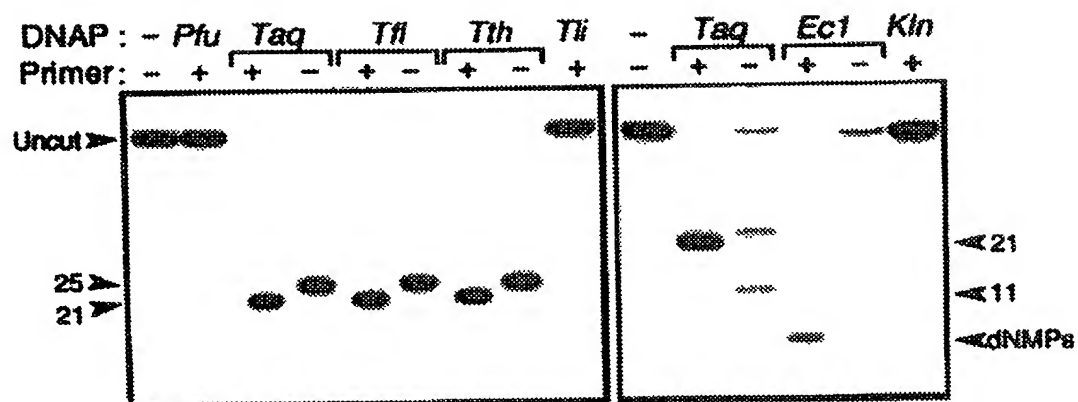
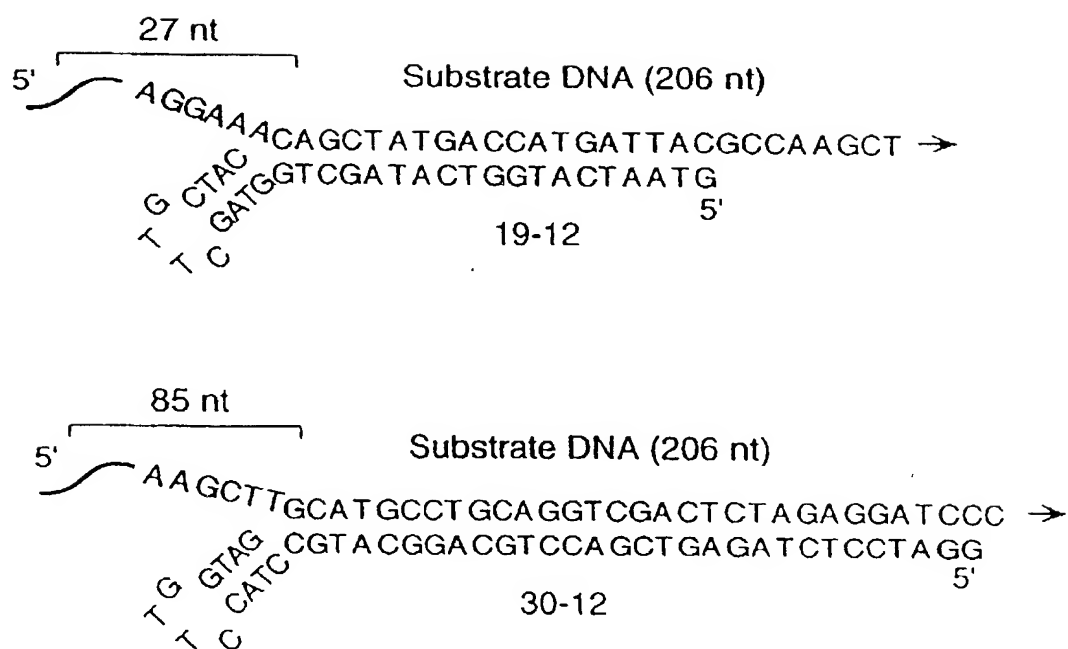
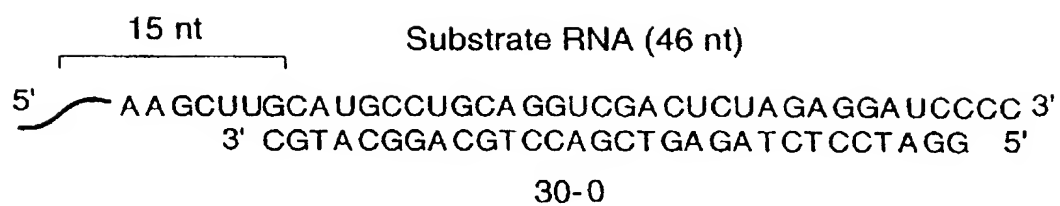


FIG. 11A

FIG. 11B

FIG. 12A





**FIG. 13A**

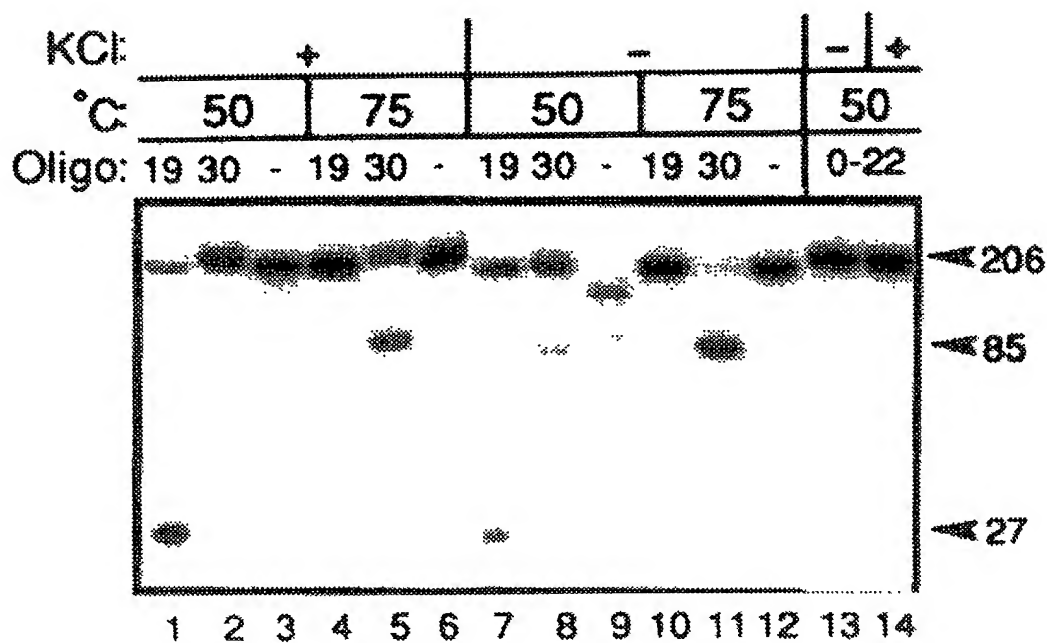


FIG. 12B

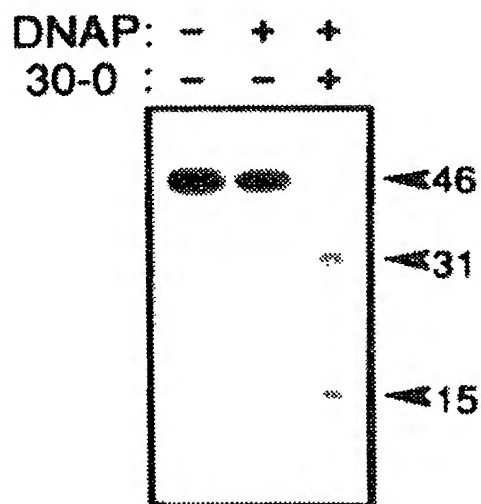
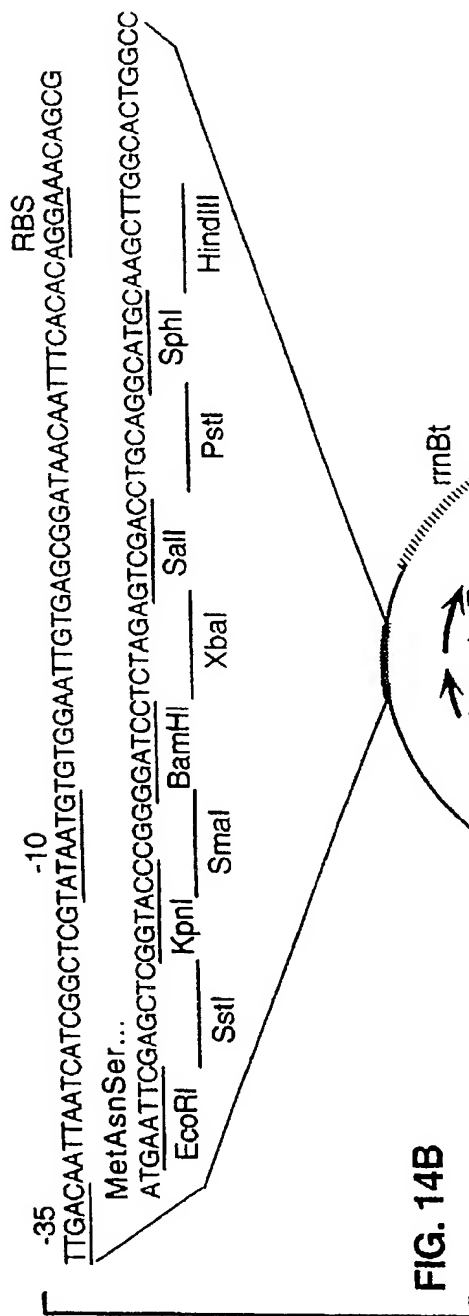
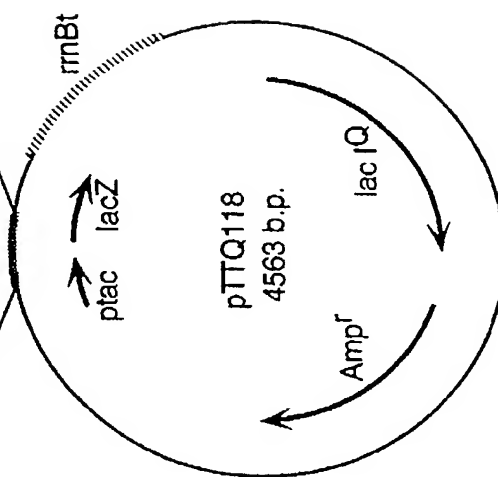


FIG. 13B





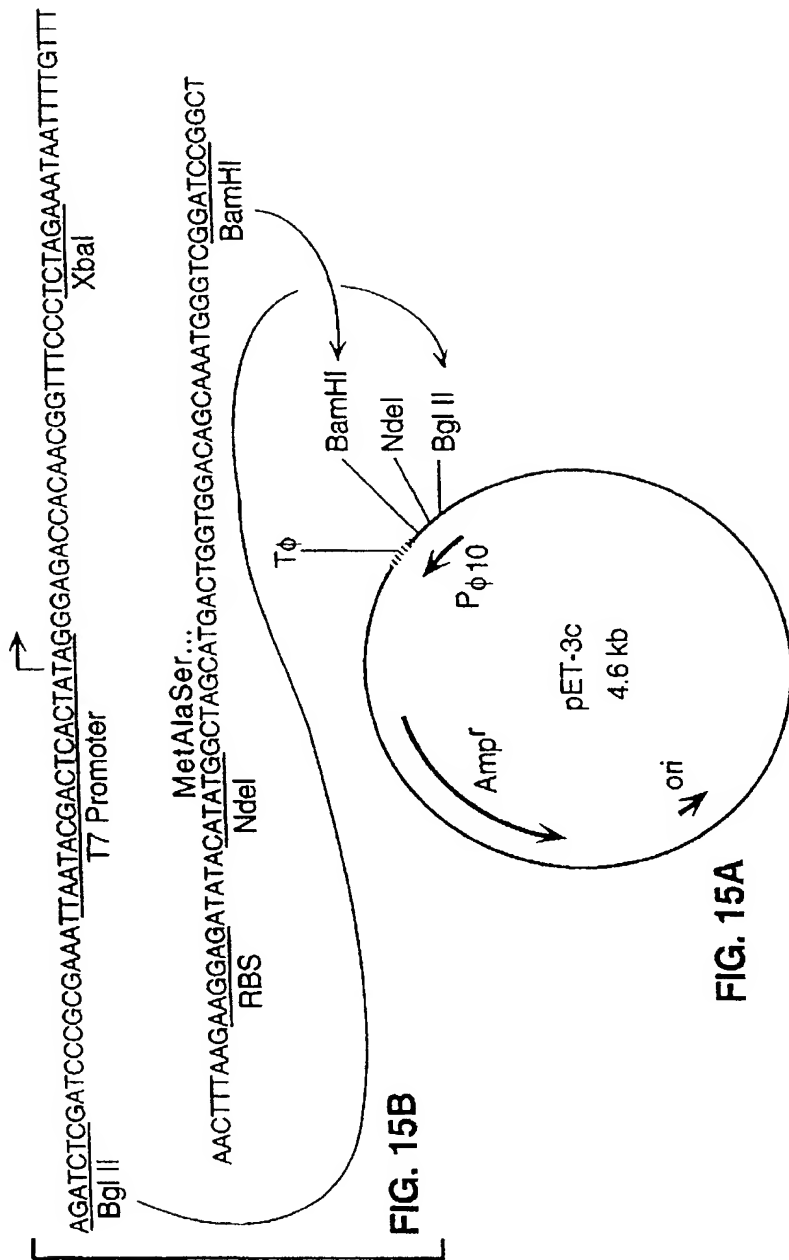
**FIG. 14B**



**FIG. 14A**

RBS: Ribosome binding site  
 ptac: Synthetic tac promoter  
 lacIQ: Lac repressor gene  
 lacZ: Beta-galactosidase alpha fragment  
 rmBt: E. coli rmB transcription terminator

**FIG. 14C**



P<sub>φ10</sub>: Bacteriophage T7 φ10 promoter  
Tφ: T7 φ Terminator  
RBS: Ribosome binding site

**FIG. 15C**

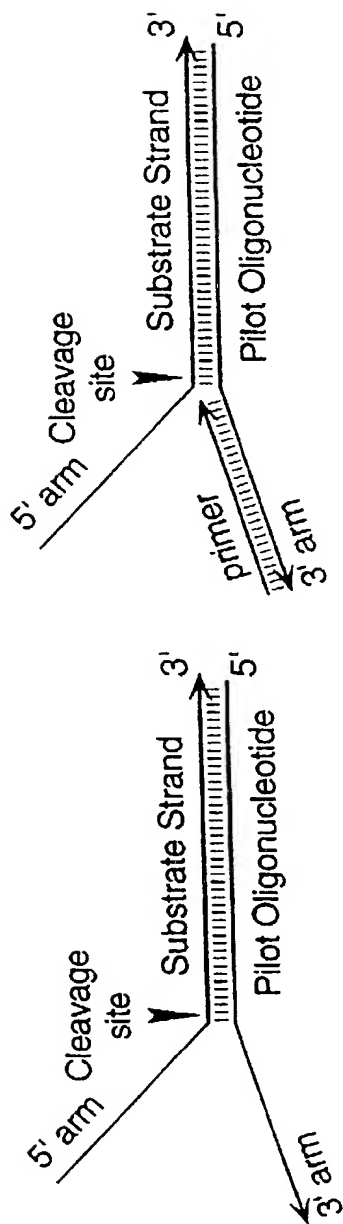


FIG. 16A

FIG. 16B

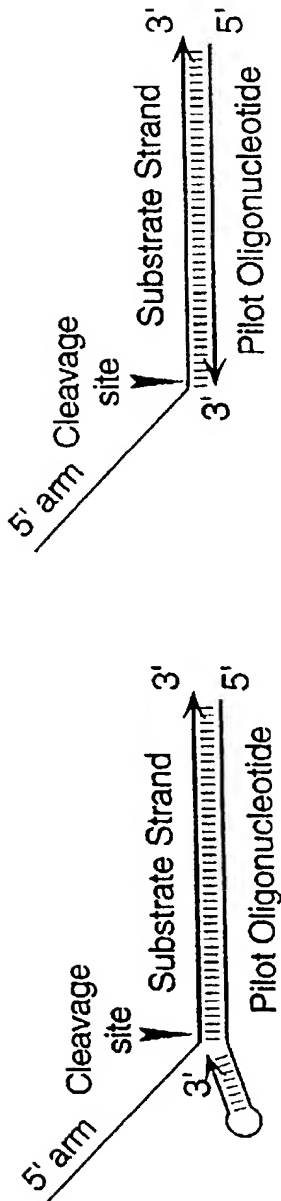


FIG. 16C

FIG. 16D

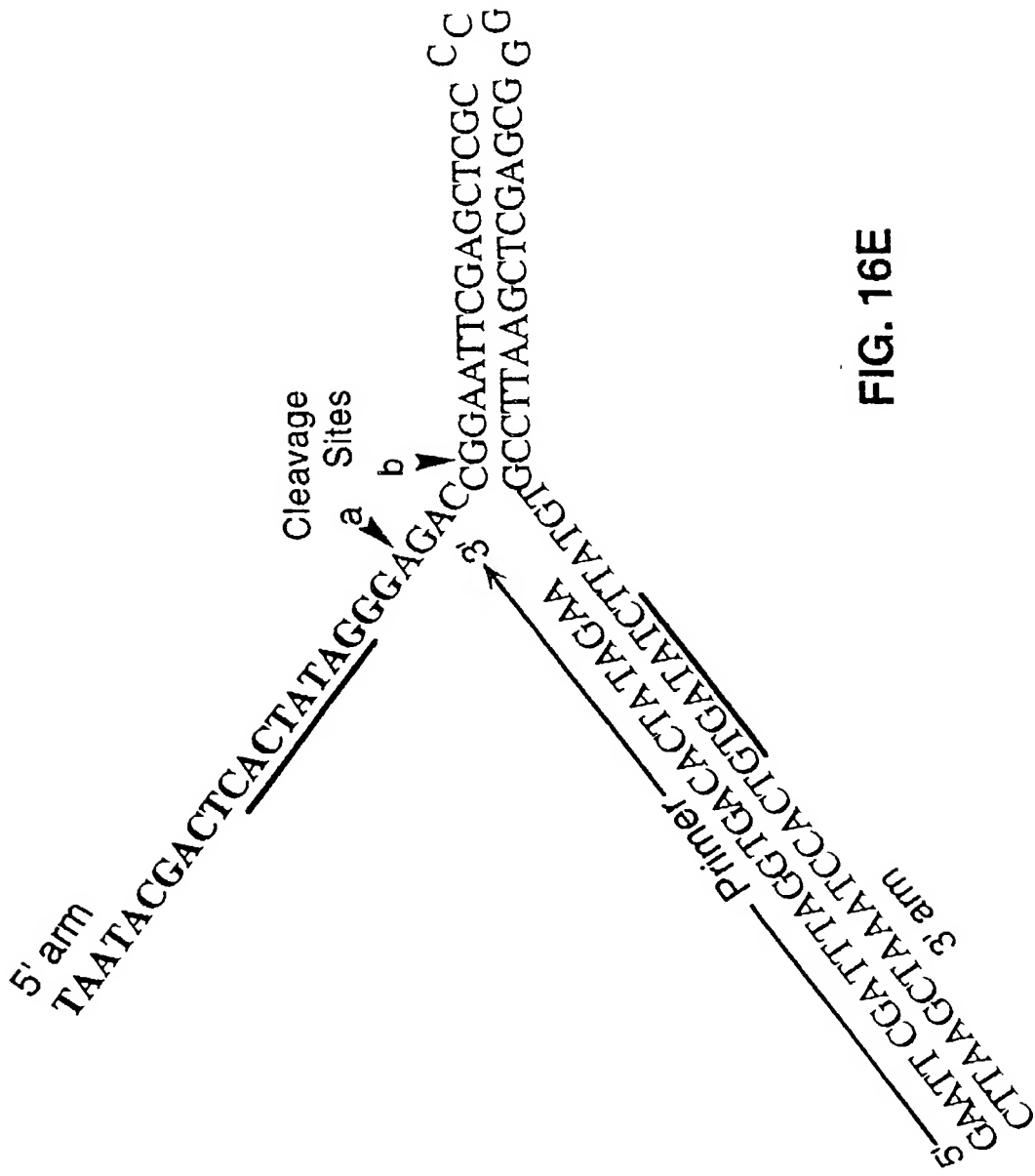


FIG. 16E

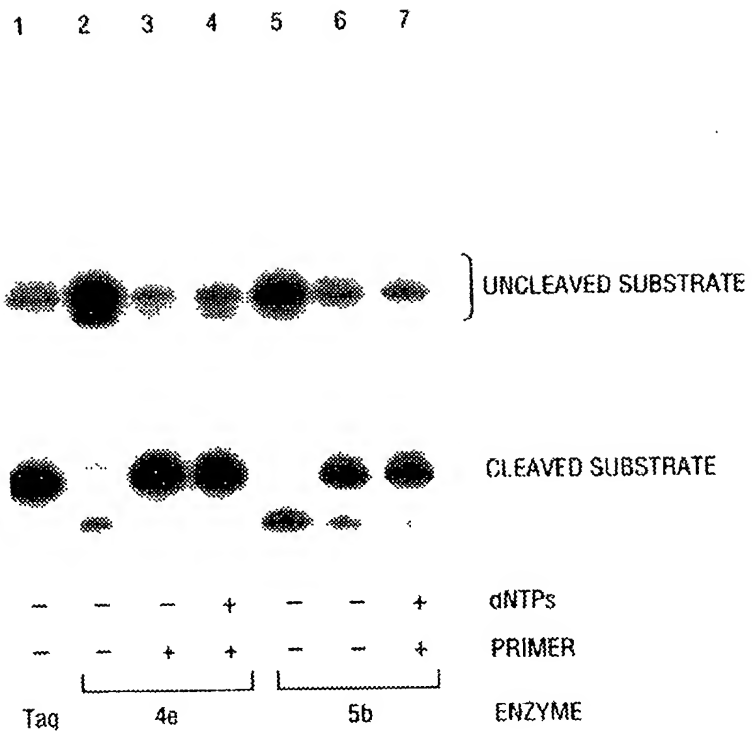


FIG. 17

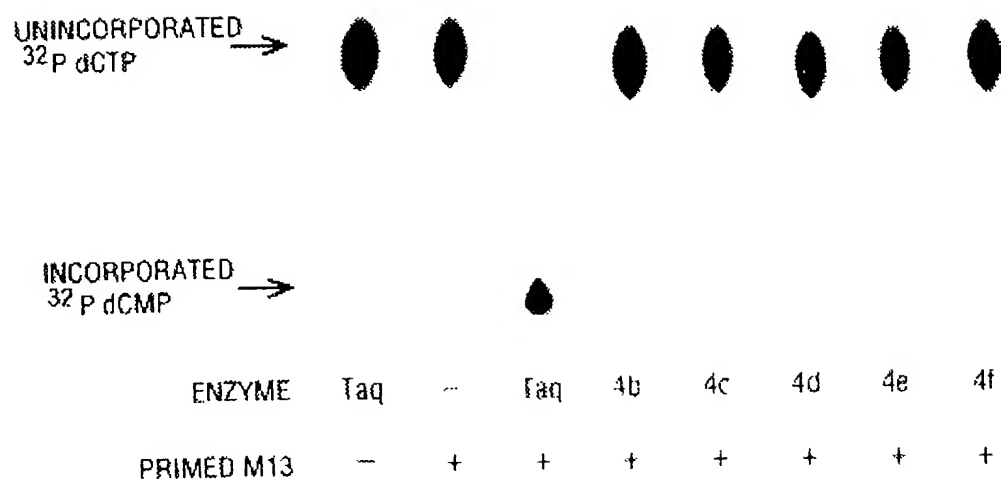


FIG. 18

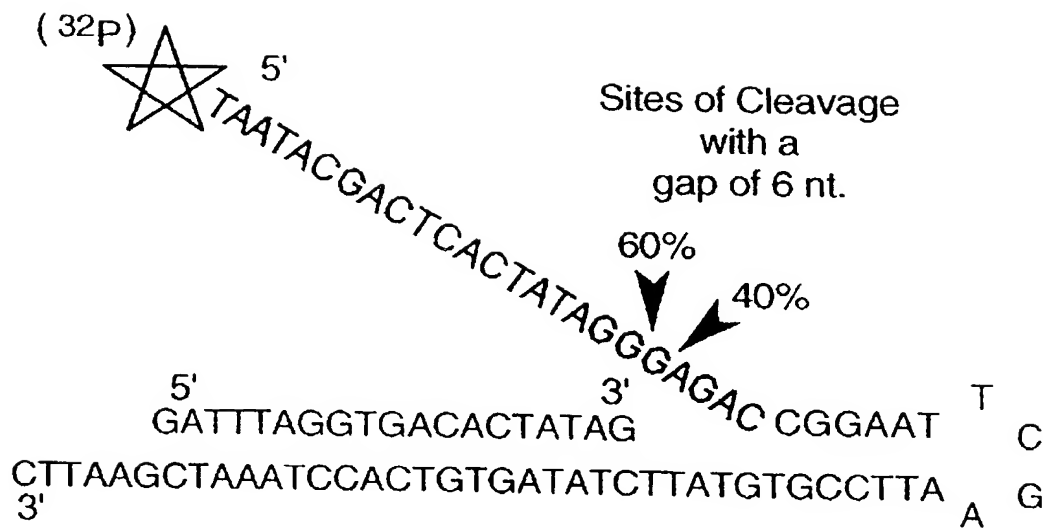


FIG. 19A

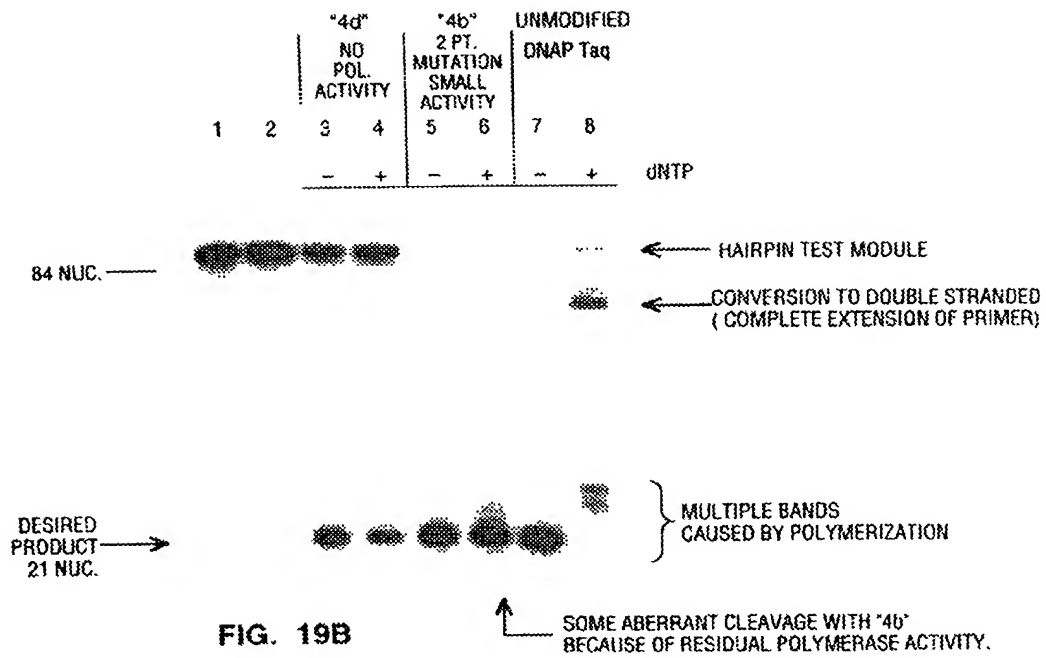


FIG. 19B

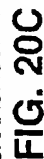




Sequence of alpha primer:

5' GACGAACAAGCGAGACAGCG 3'

**FIG. 20B**



*Ban* II  
*Sst* I  
*Asp* 718  
*Ava* I  
*Kpn* I  
*Xma* I  
*Sma* I  
*Bam* HI XI  
*EcoR* I

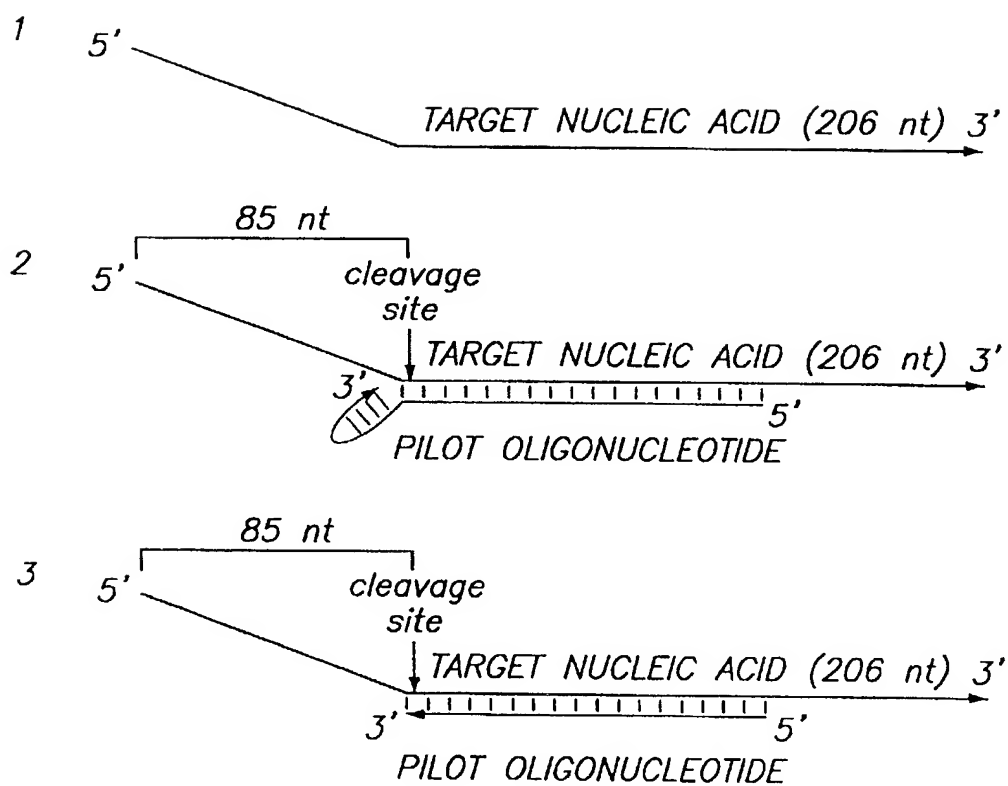
CGCCAGGGTTTTCCAGTCACGAGTGTGTAACACGCGCCAGTGAAATTGTAATACGACTCACTATAGGGCGAAATTCGAGCTCGGTACCGGGGATCCTC  
 GCGGTCCCAAAAGGGTCAGTGTGCAACATTTTGCTGCCGGTCACTTAACATTATGCTGAGTGATATCCGGCTTAAGCTCGAGGCCATGGGCCCTAGGAG

———— 47 Forward ————  
 ———— 17 ————  
 ———— Pilot 30-0 ————

[illegible]

TCCGGT|CACAATTCCACACACATACGA  
 228  
 AGCGAGTGTTTAAGGTGTTCTATGCT  
 ---48 Reverse  
 206

FIG. 21

**FIG. 22A**

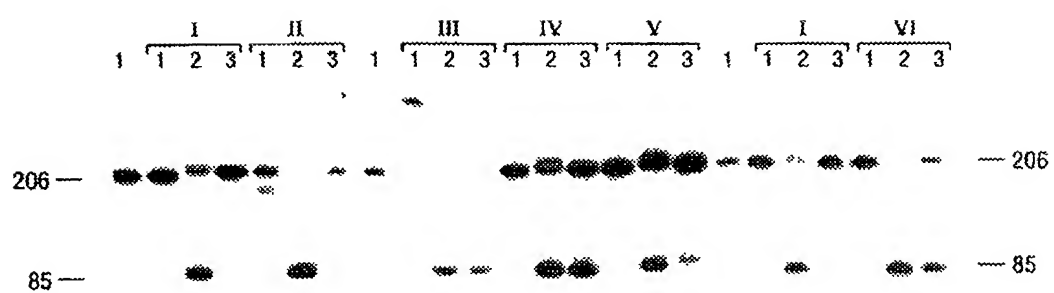


FIG. 22B

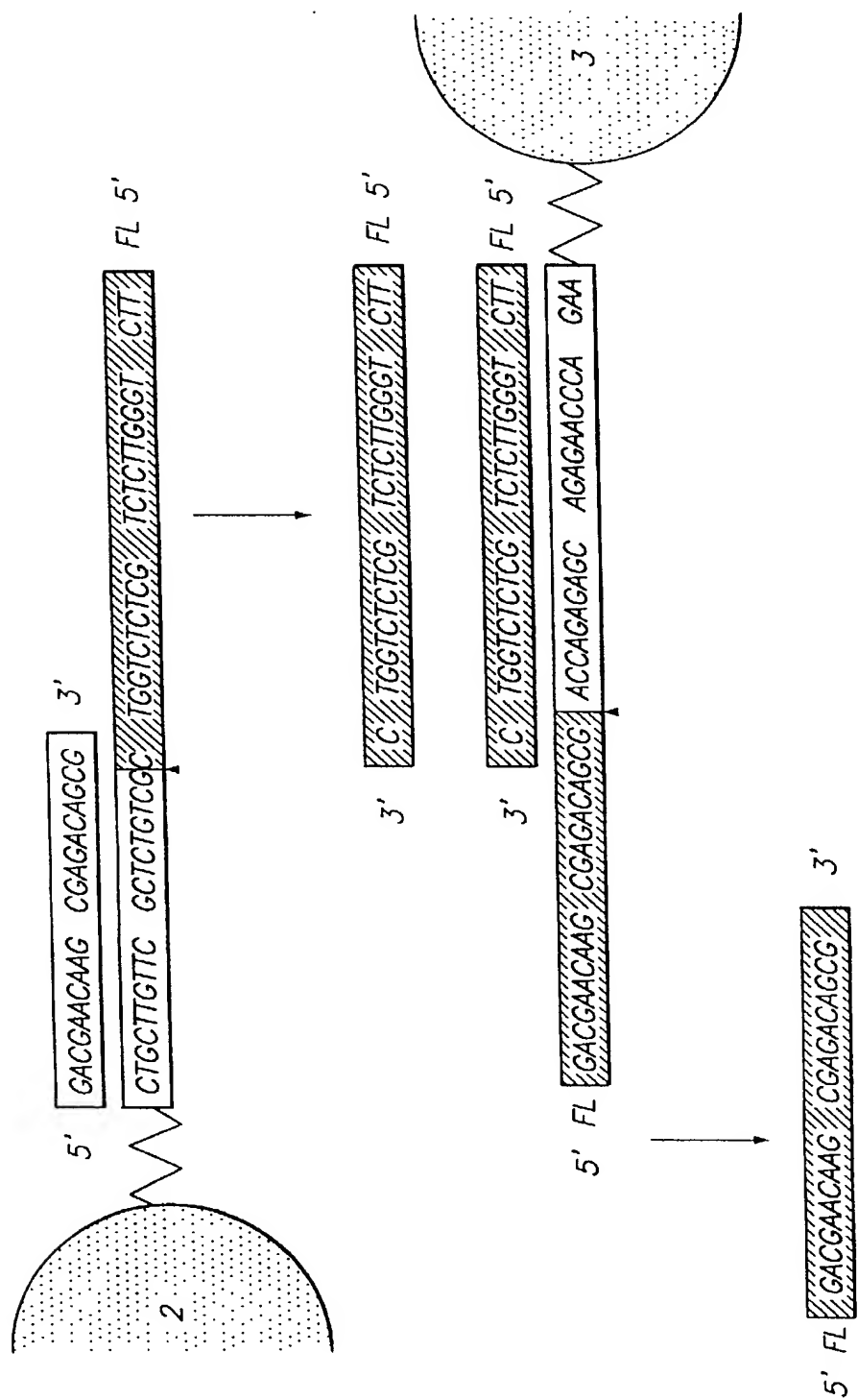


FIG. 23

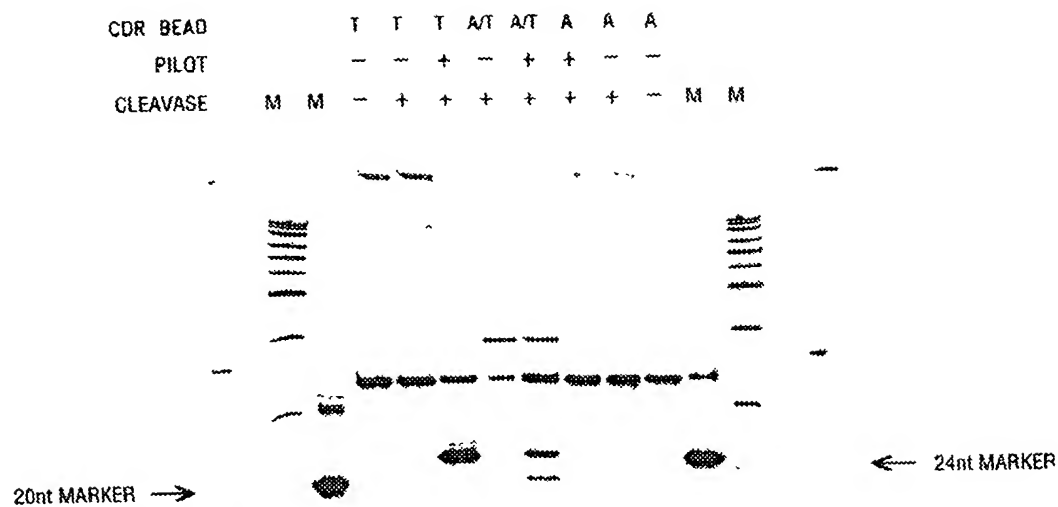


FIG. 24

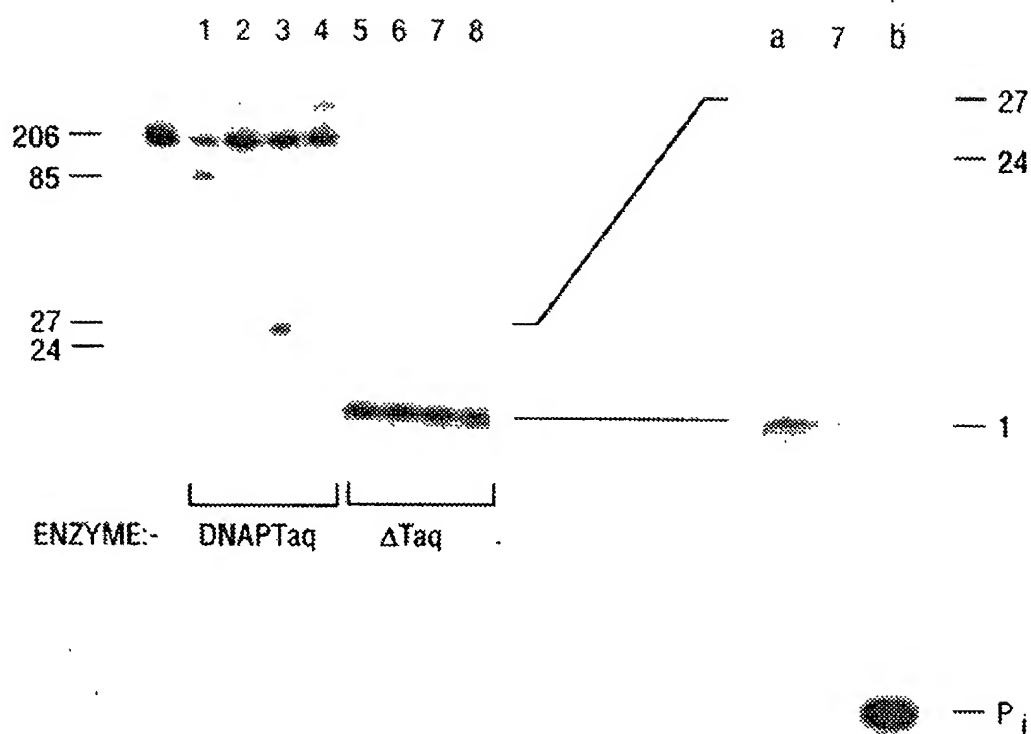


FIG. 25A

FIG. 25B

FIG. 26A

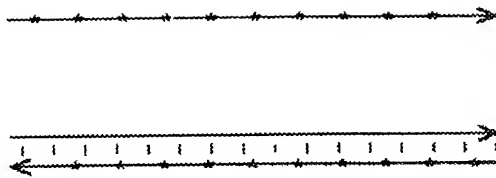
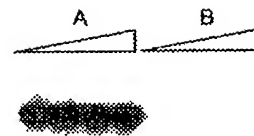
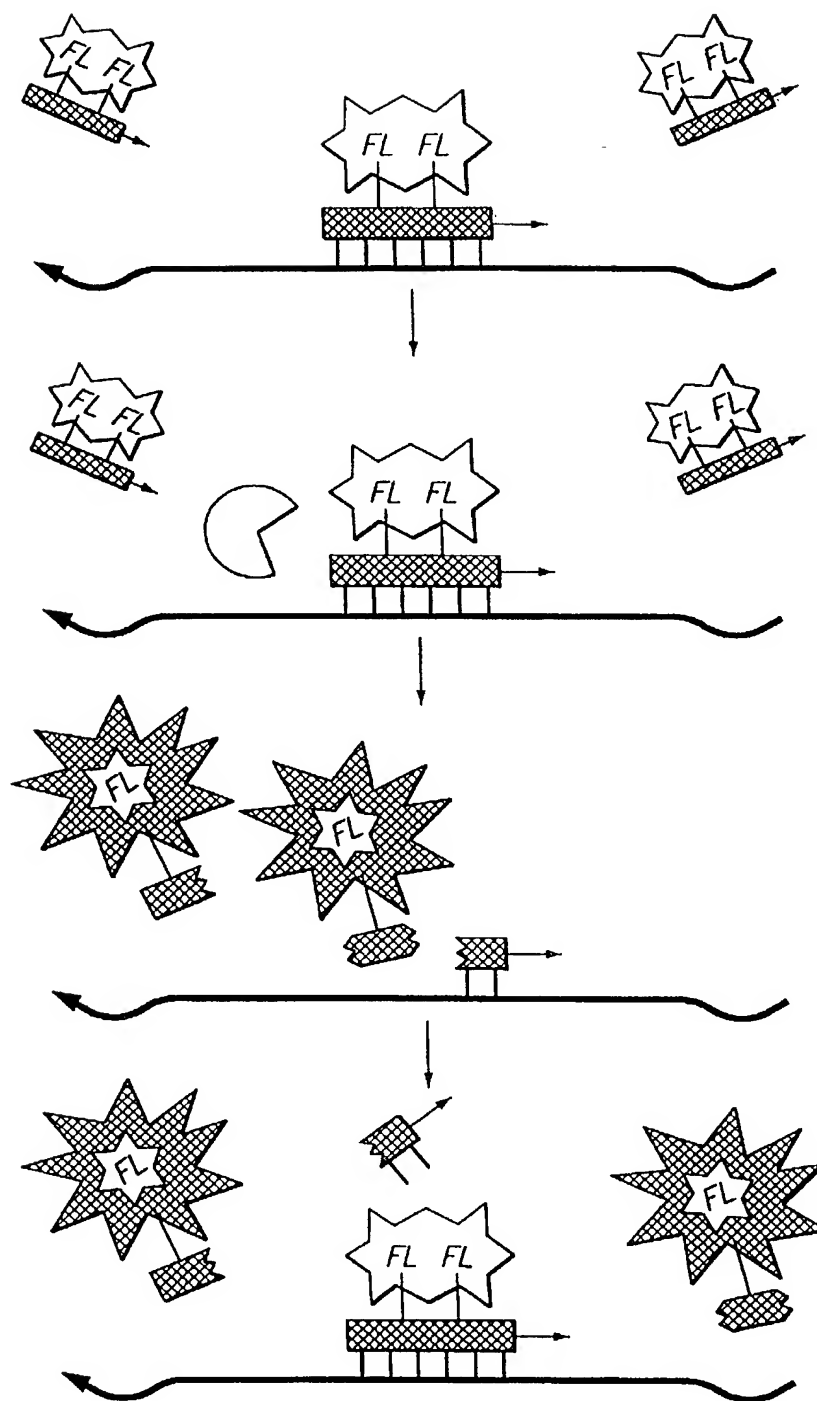


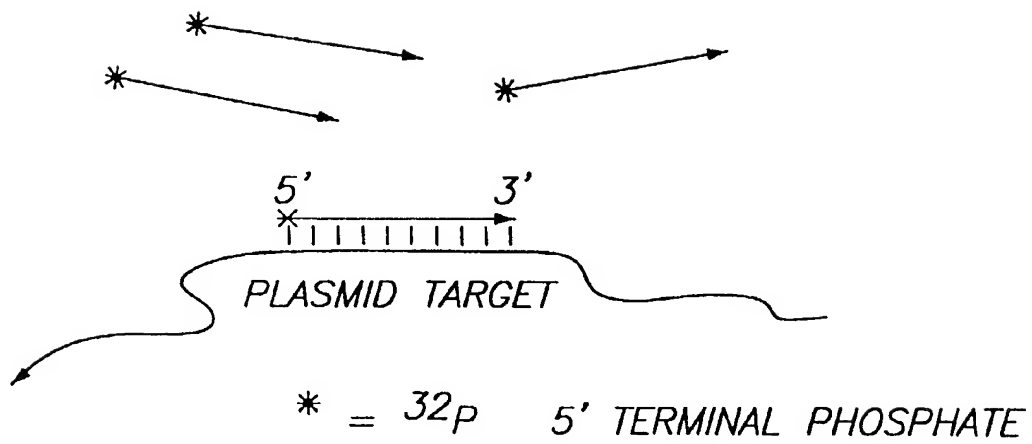
FIG. 26B

\* = 32p

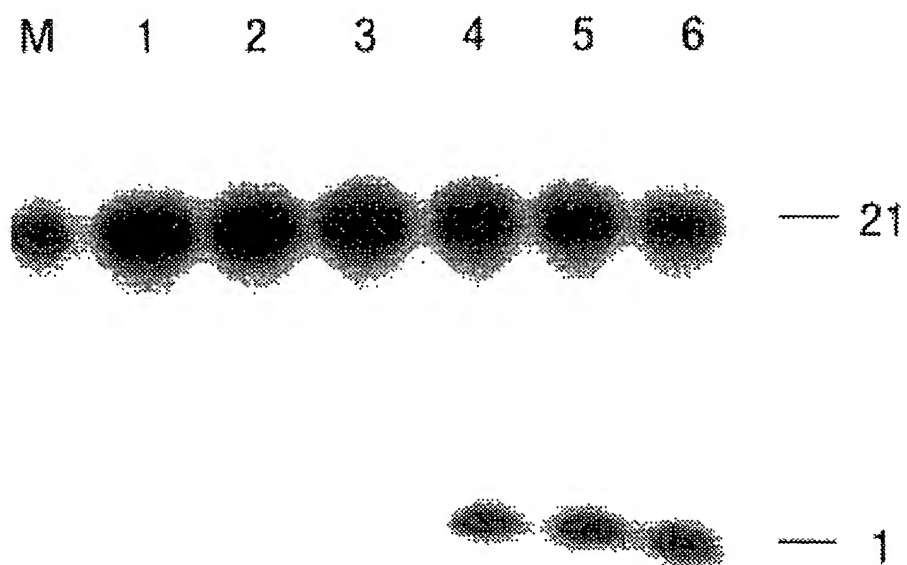




**FIG. 27**



**FIG. 28A**

**FIG. 28B**

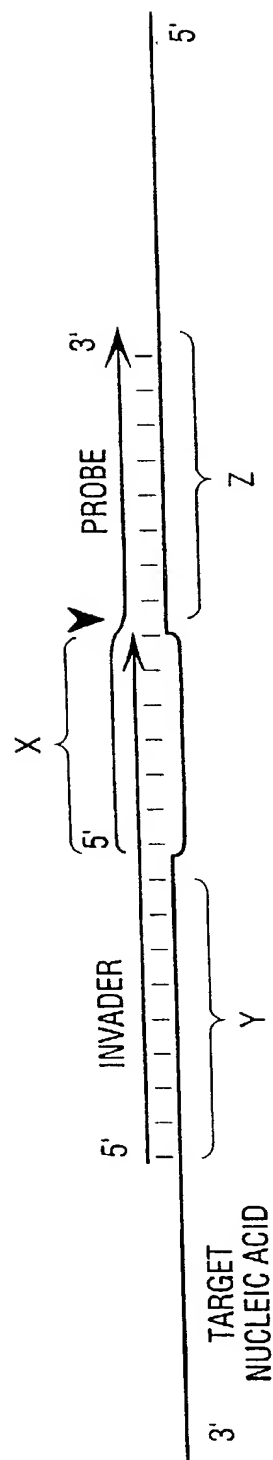
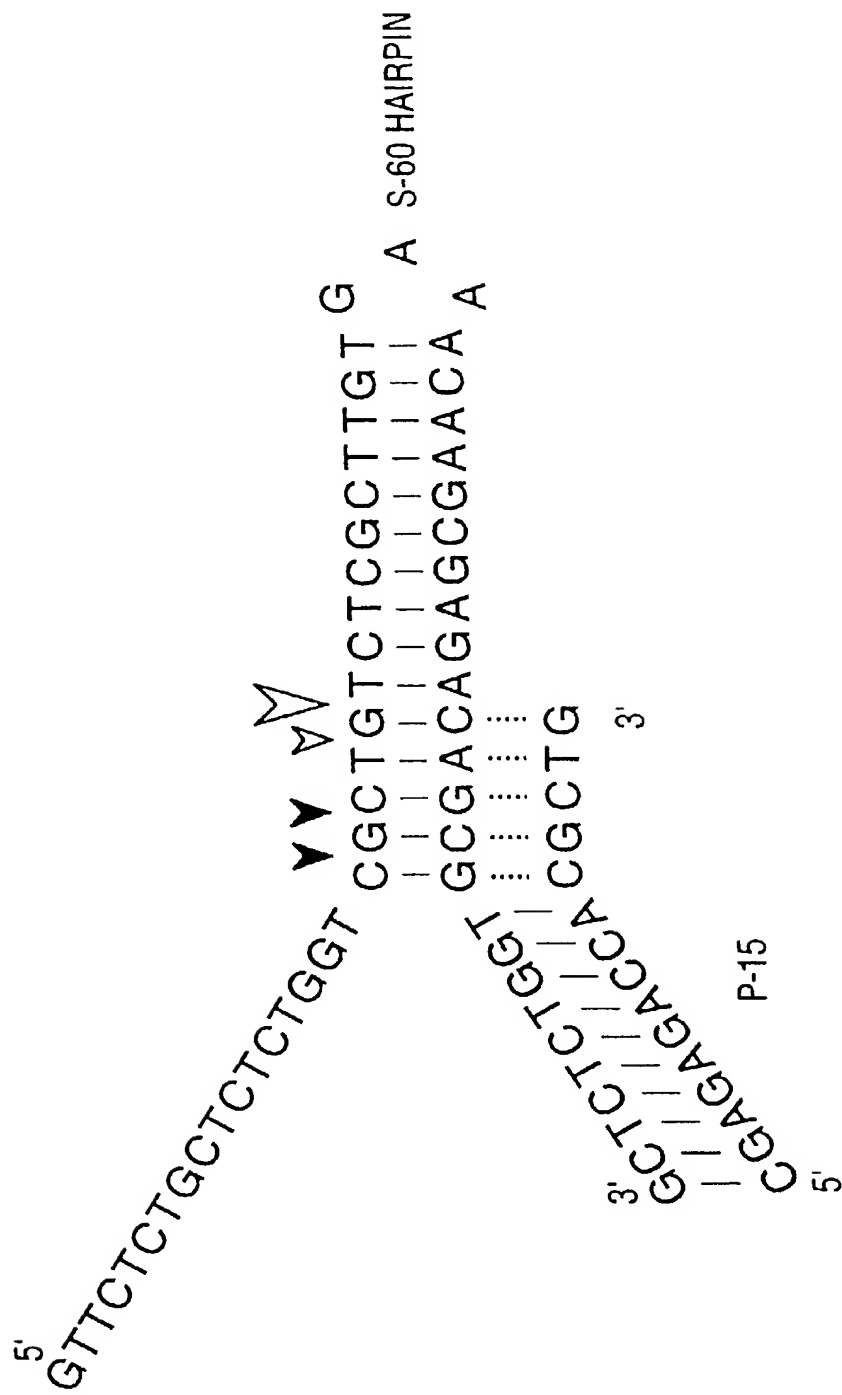
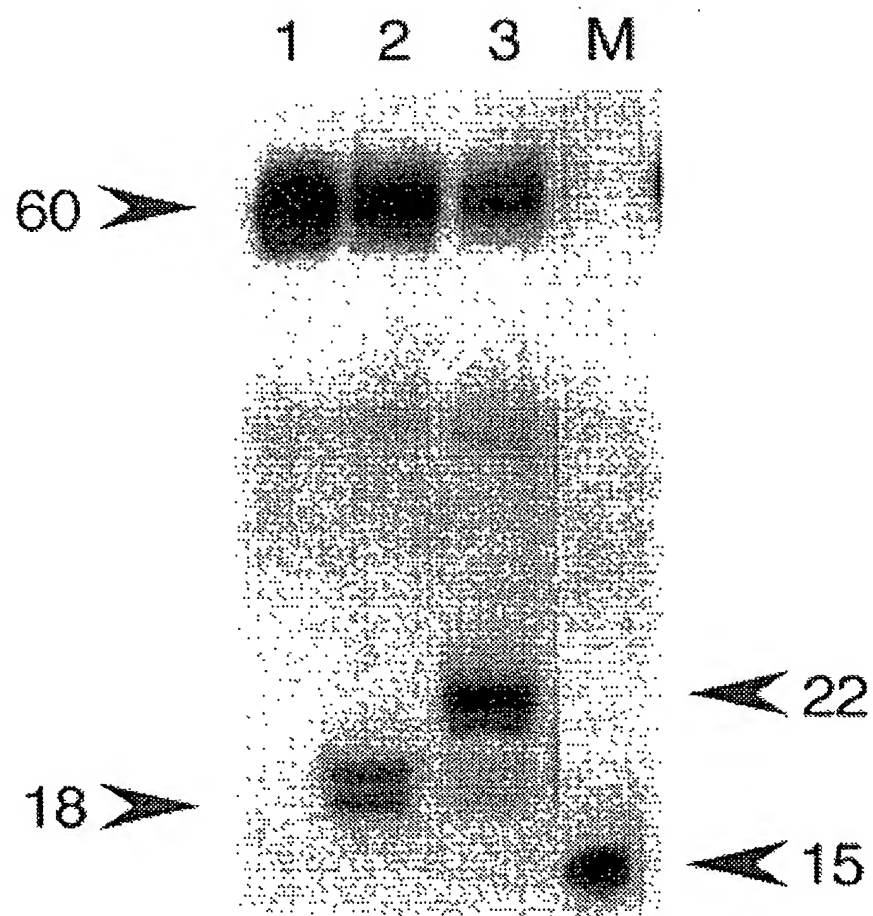


FIG. 29



**FIG. 30**

**FIG. 31**

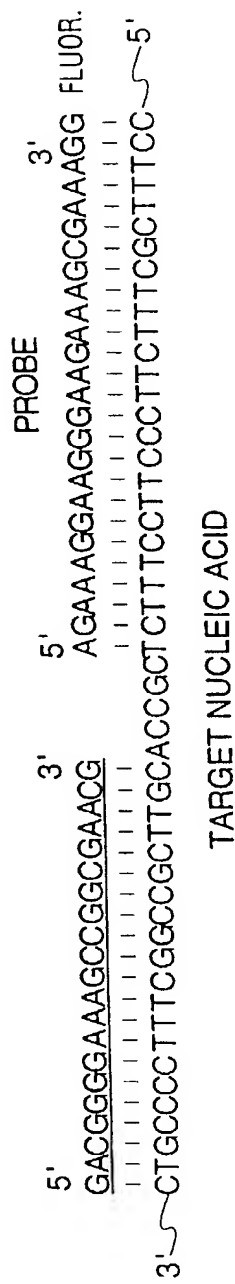


FIG. 32A

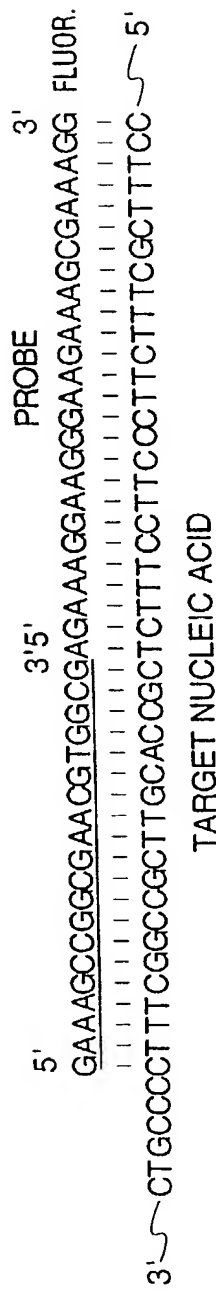


FIG. 32B

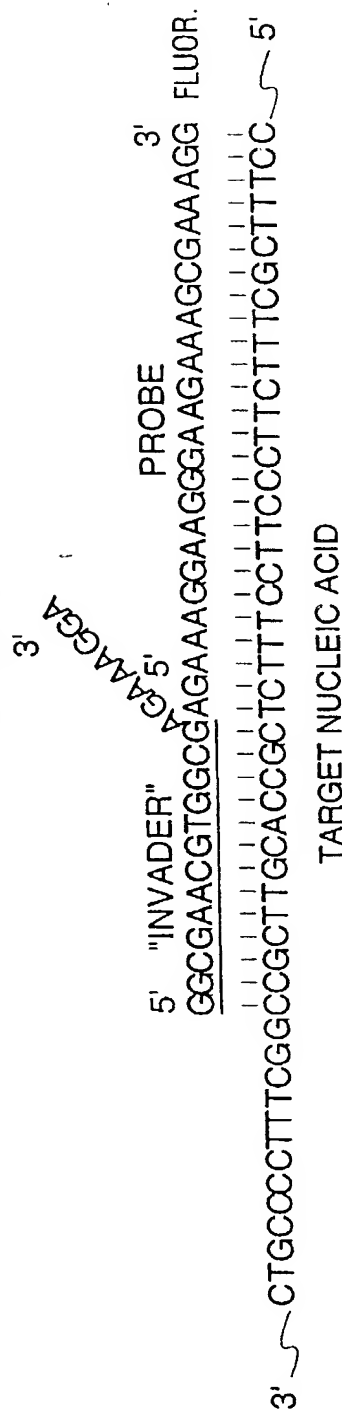


FIG. 32C

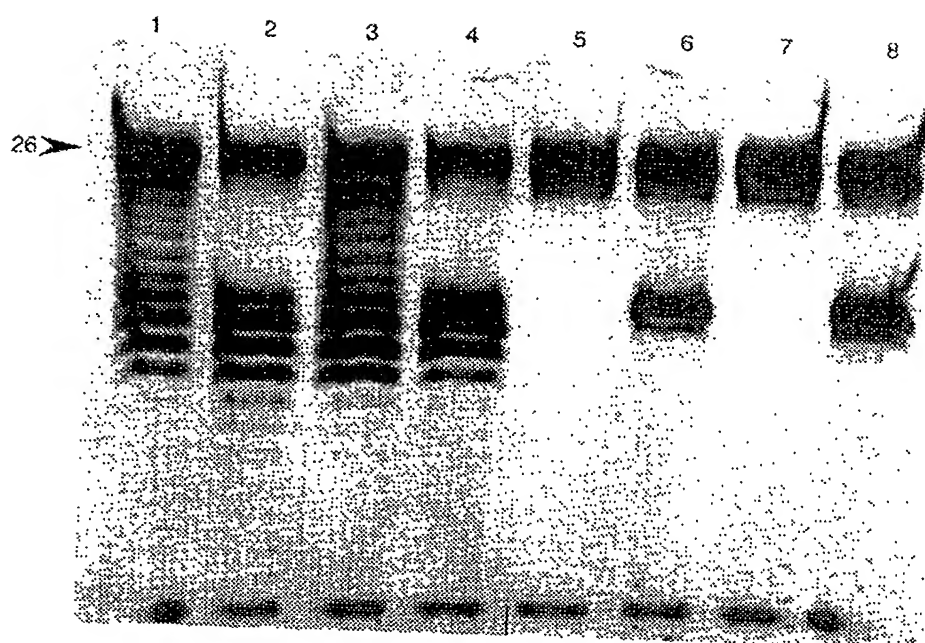


FIG. 33



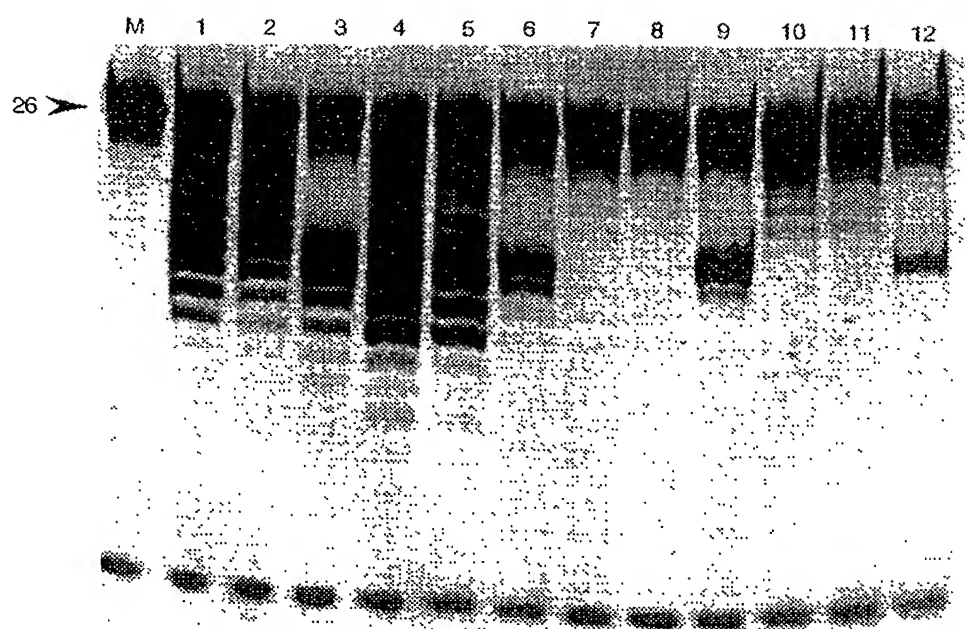


FIG. 34

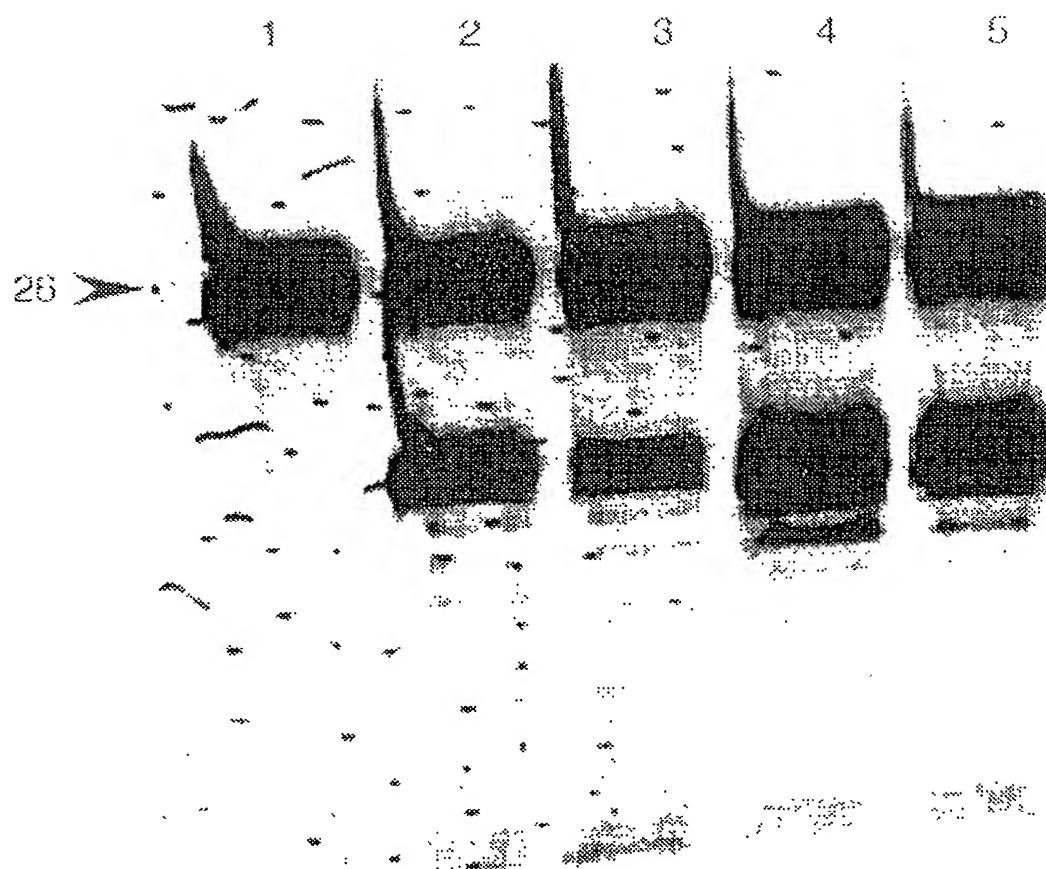


FIG. 35

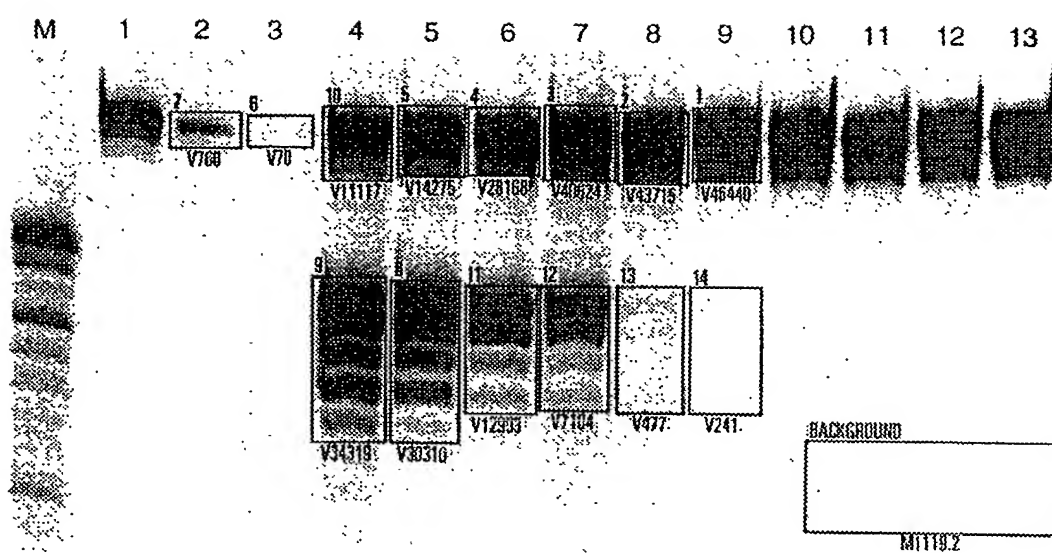


FIG. 36

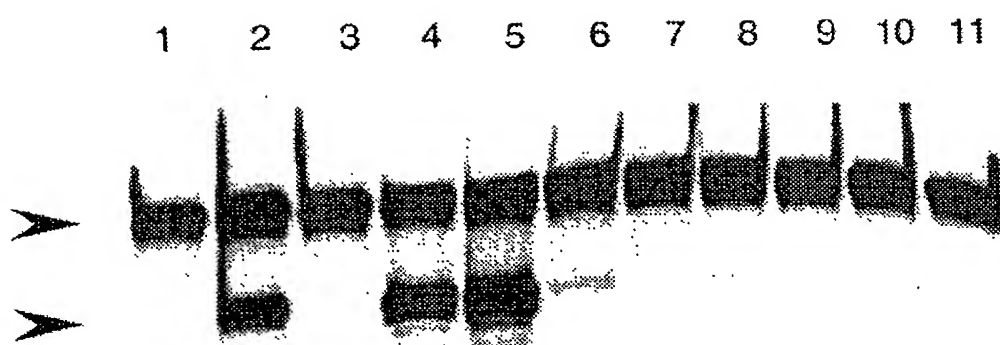
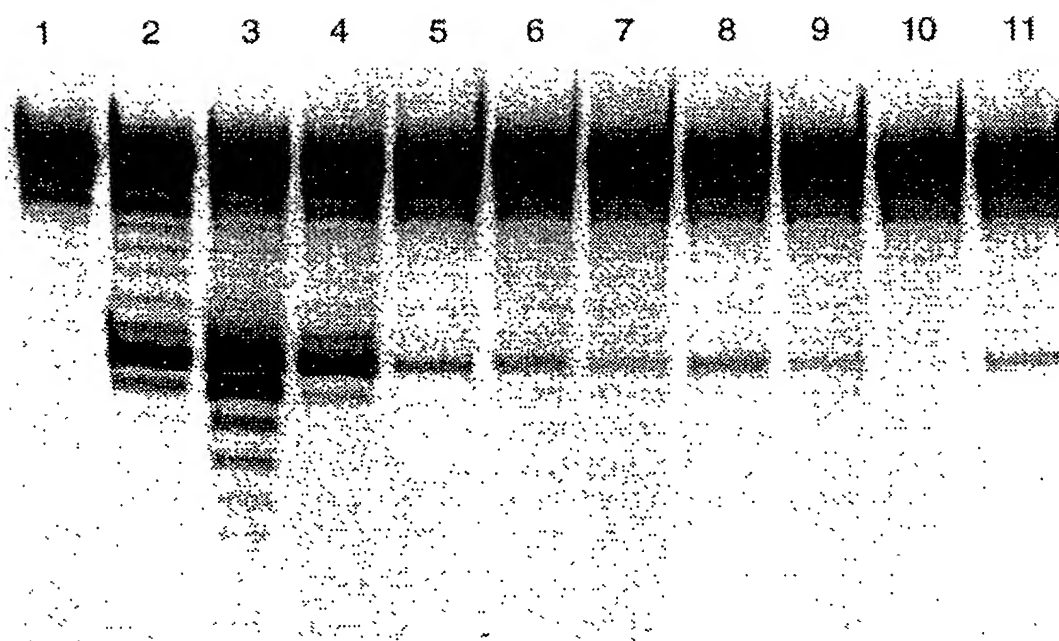
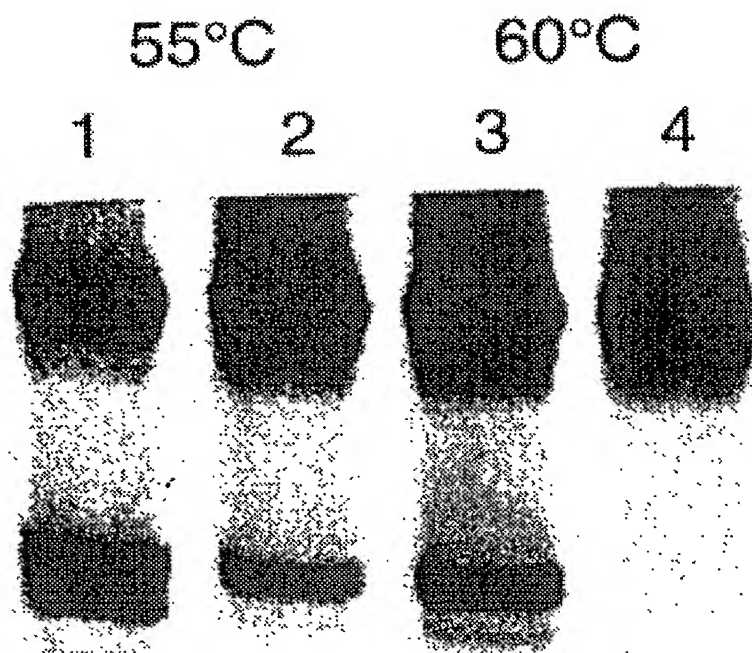


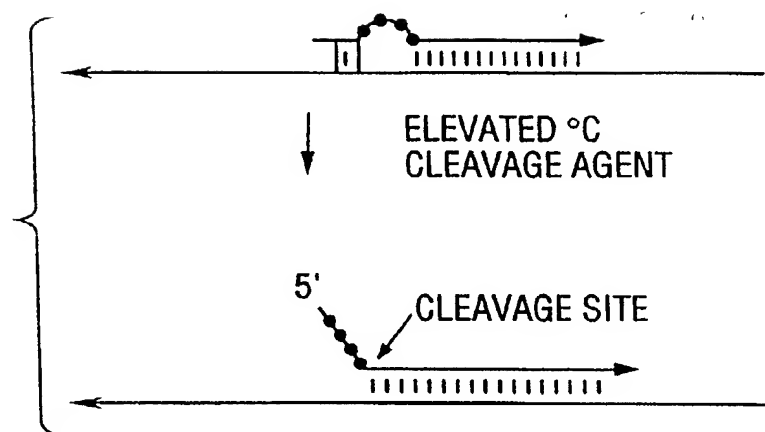
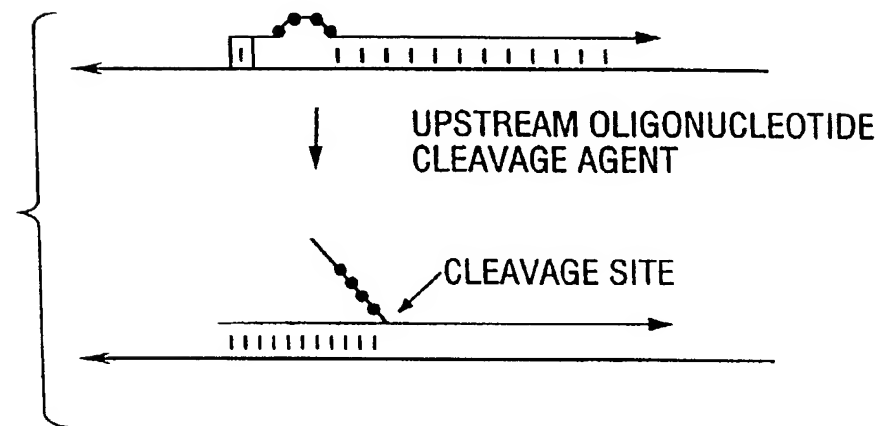
FIG. 37



**FIG. 38**



**FIG. 39**

**FIG. 40A****FIG. 40B**

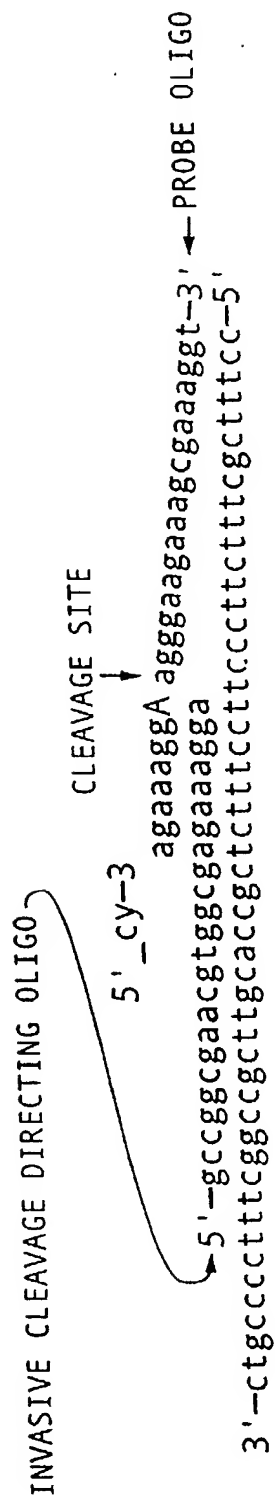
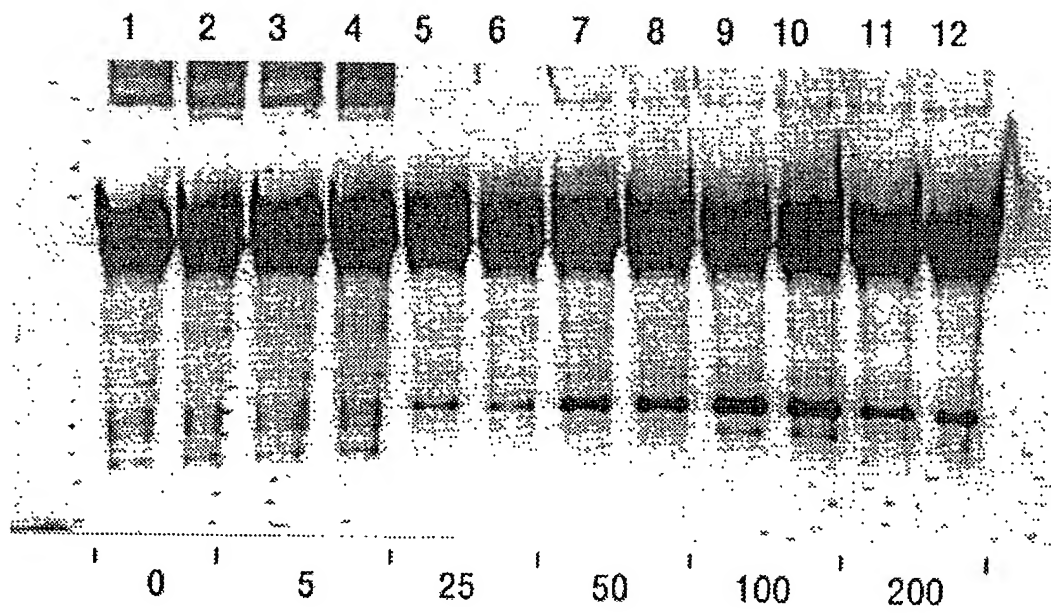


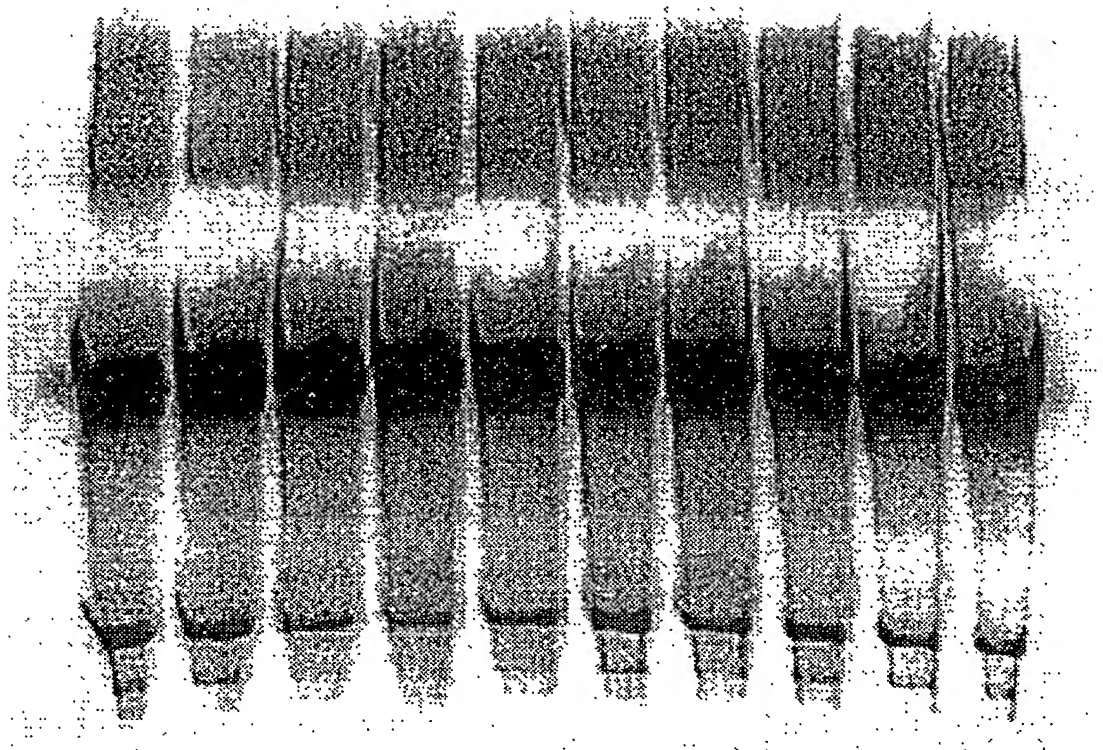
FIG. 41





**FIG. 42**

1 2 3 4 5 6 7 8 9 10



**FIG. 43**

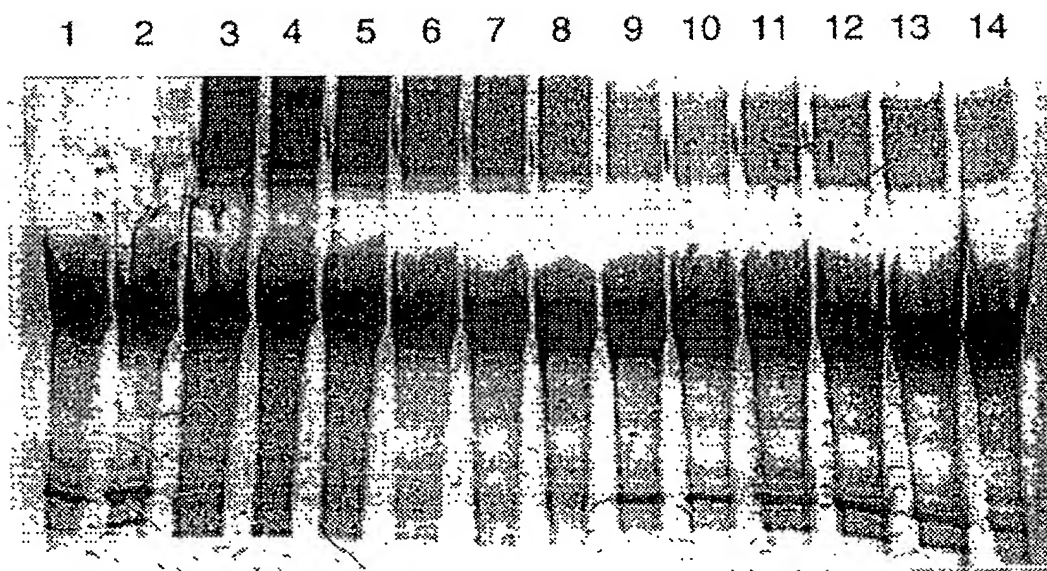


FIG. 44

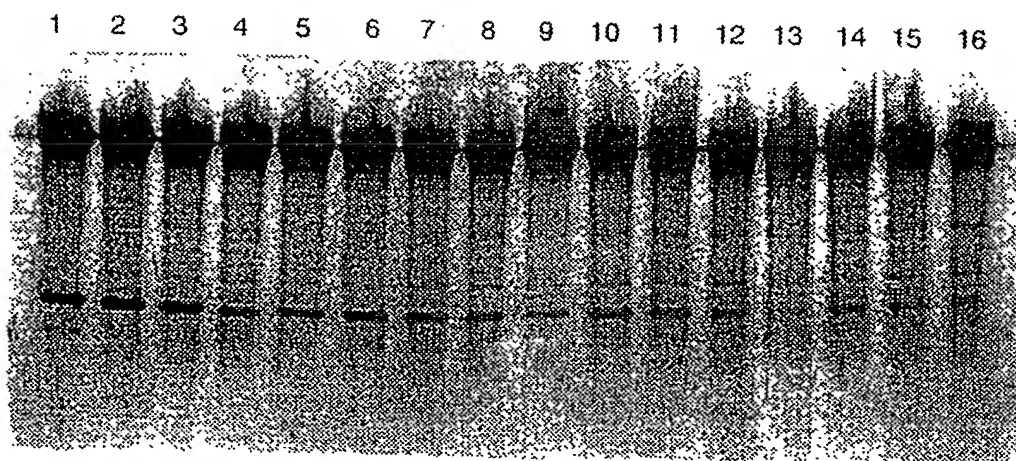


FIG. 45

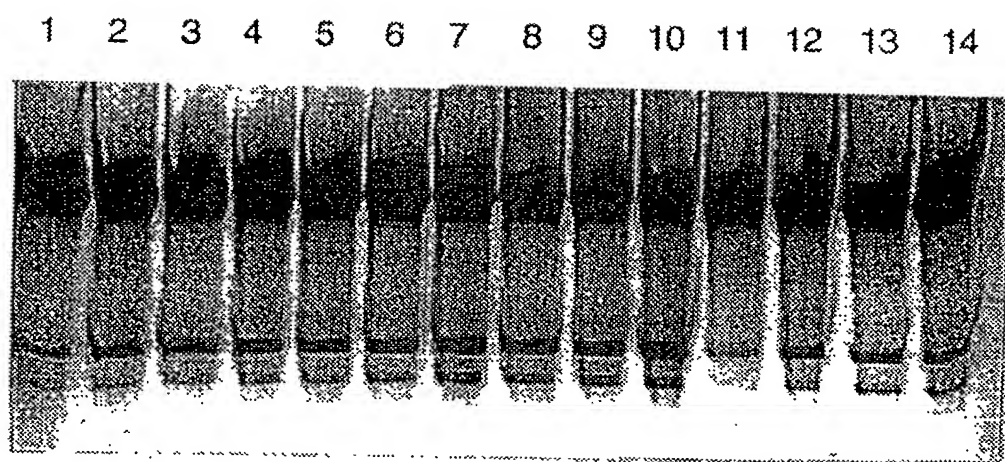


FIG. 46

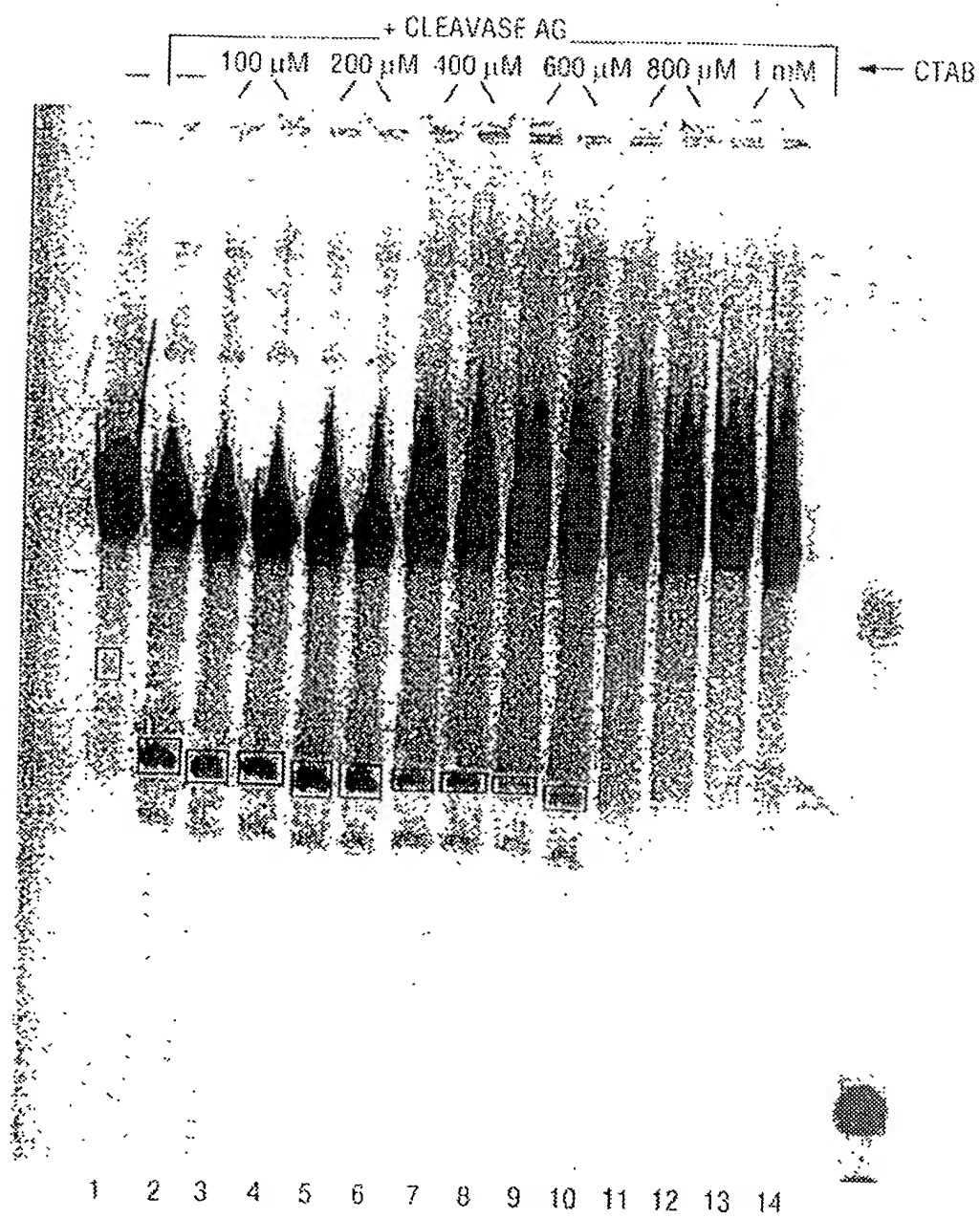
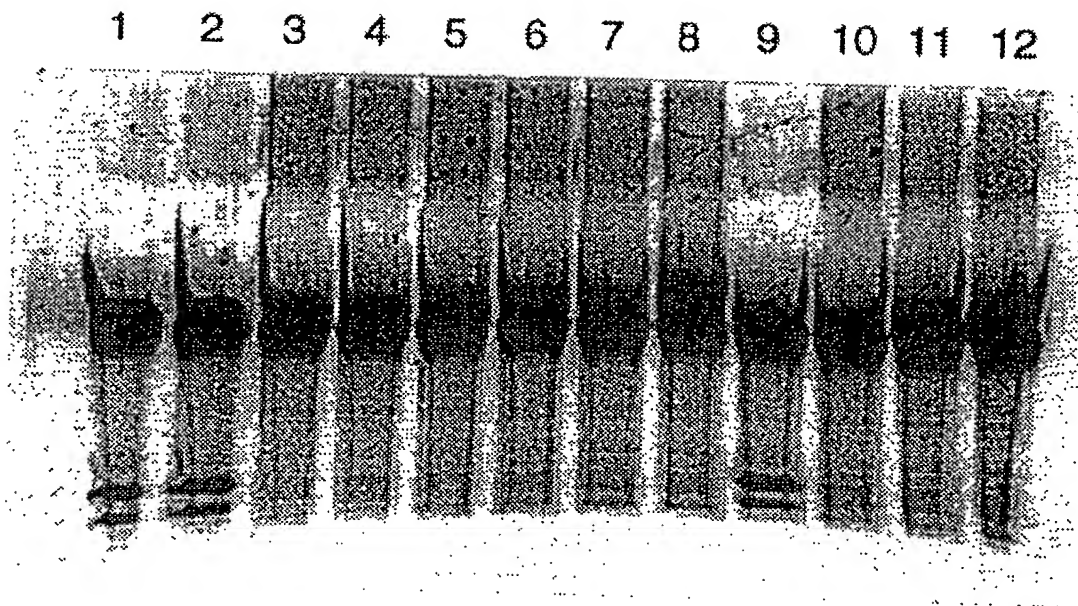
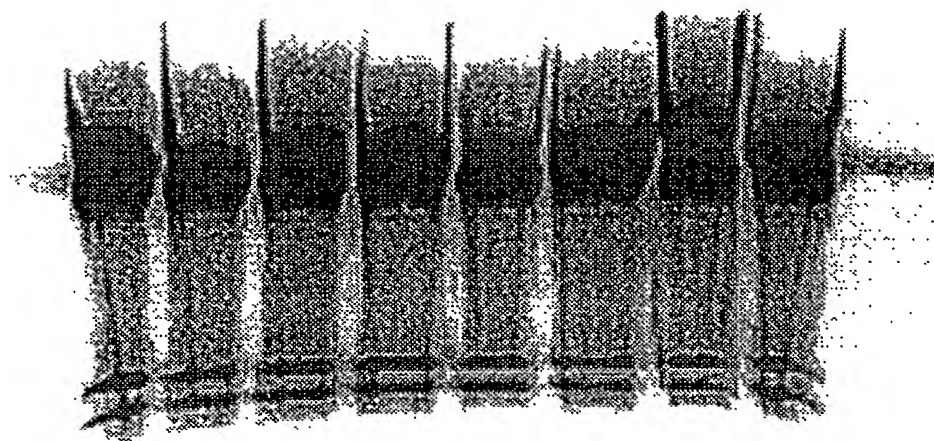


FIG. 47



**FIG. 48**

1 2 3 4 5 6 7 8



**FIG. 49**



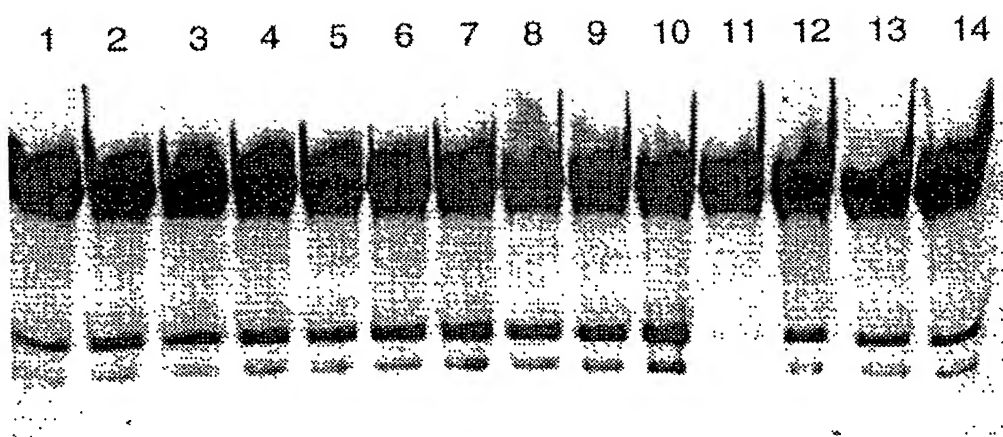
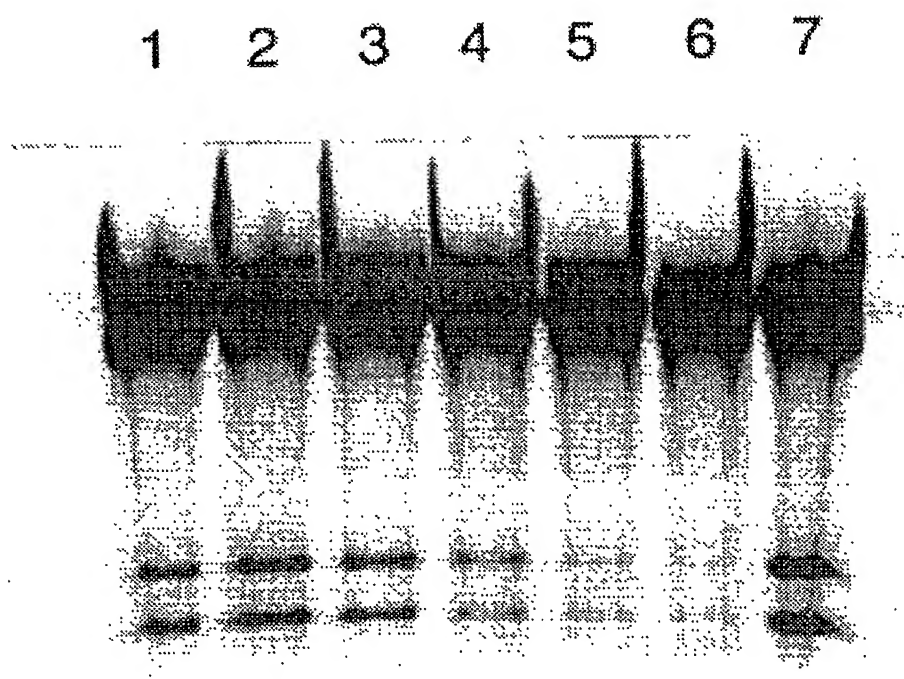


FIG. 50



**FIG. 51**

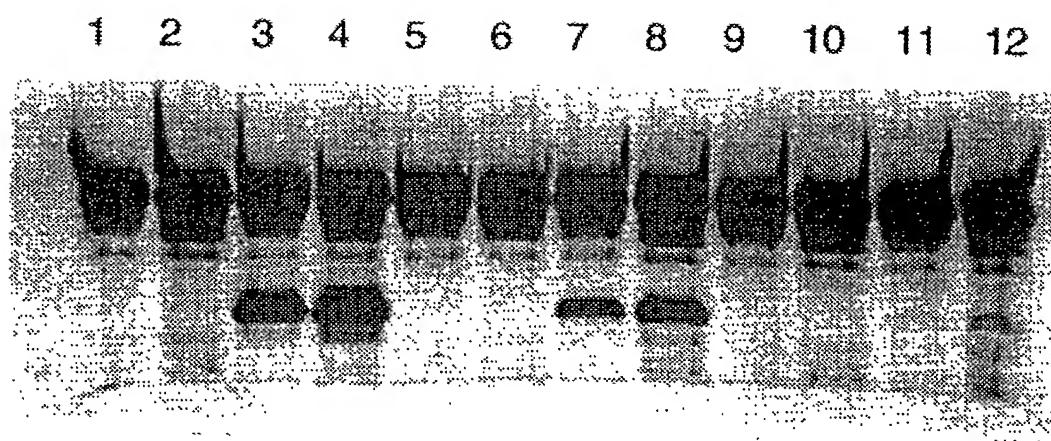
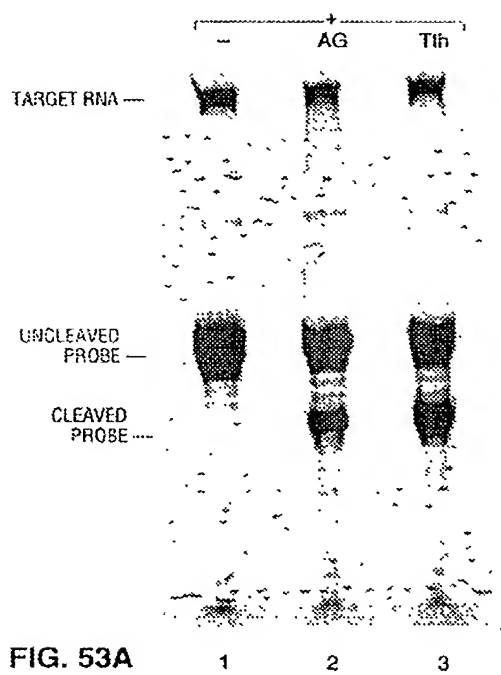


FIG. 52



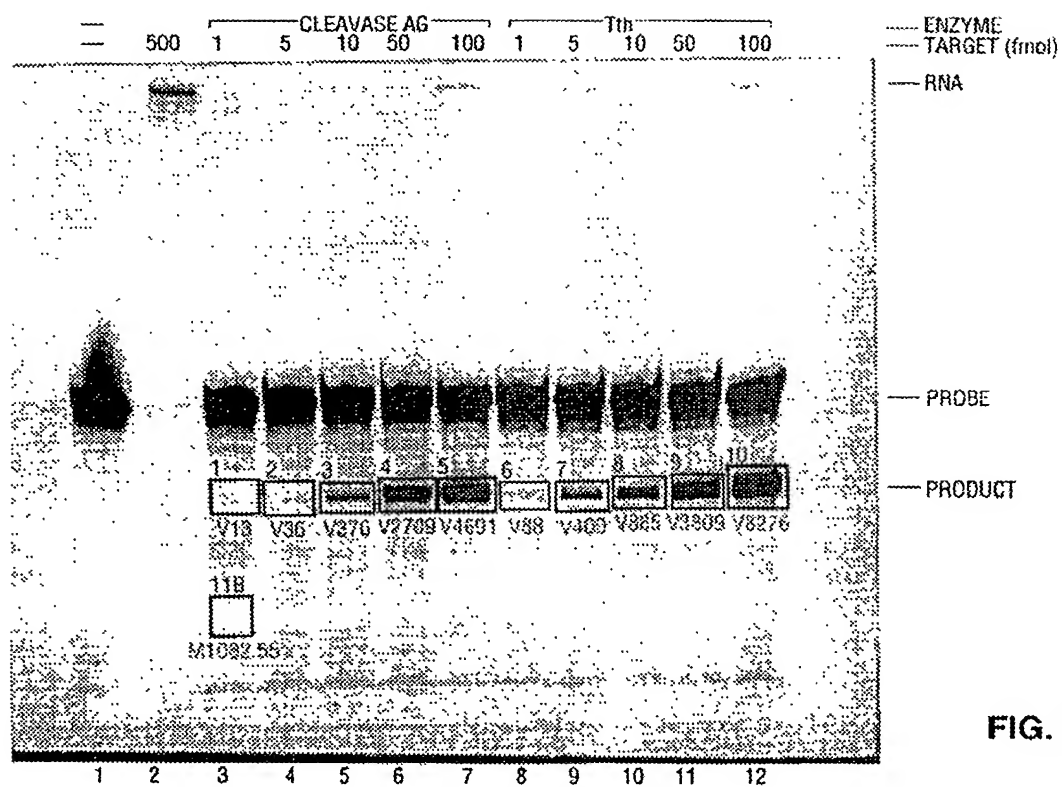
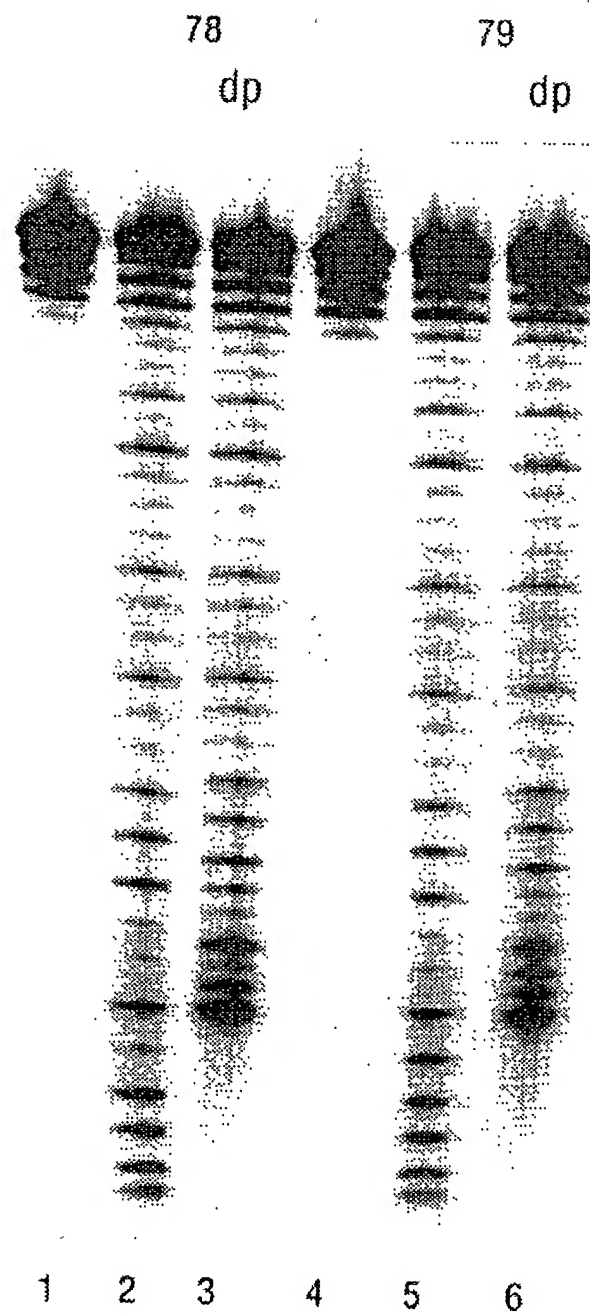


FIG. 54

**FIG. 55**

70 (C10 amino T's)  
74 (C6 amino T's)

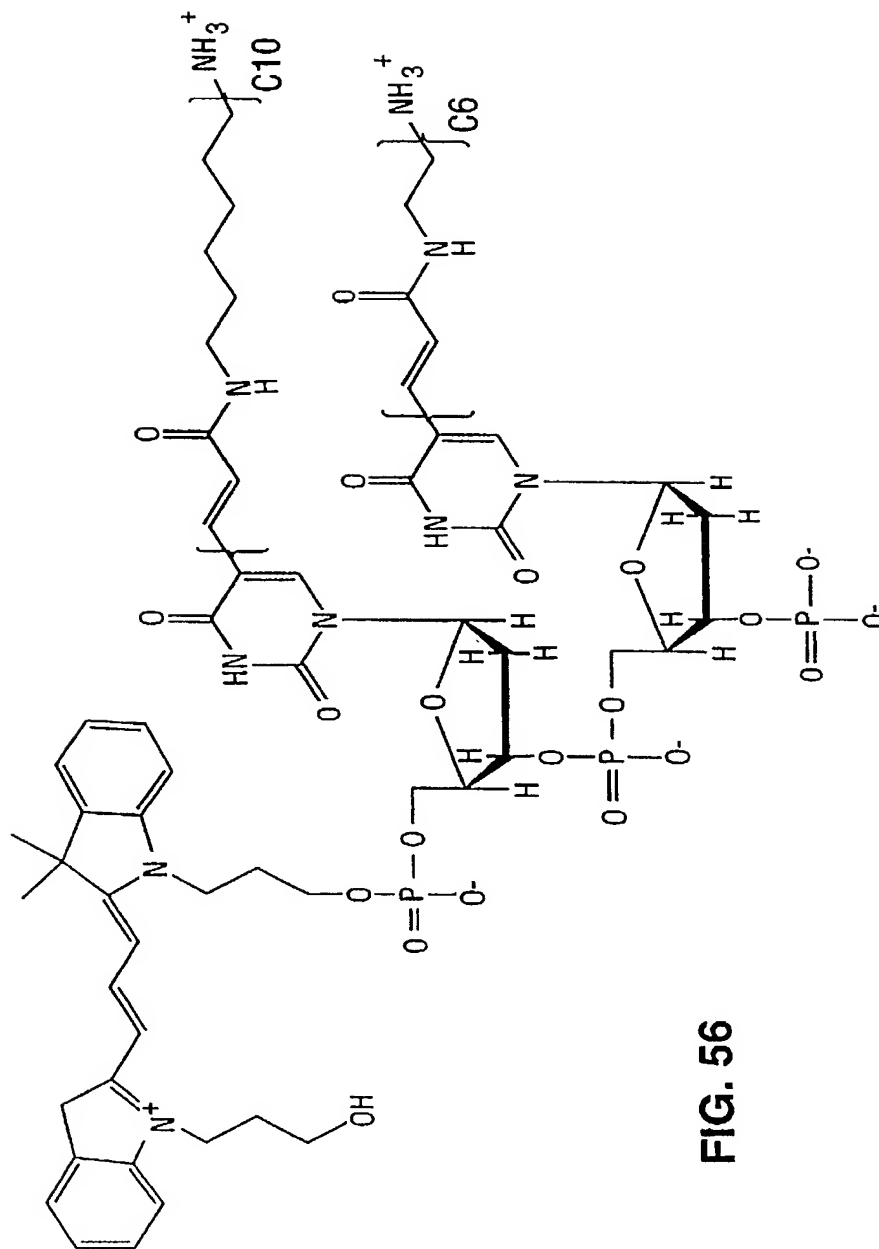


FIG. 56

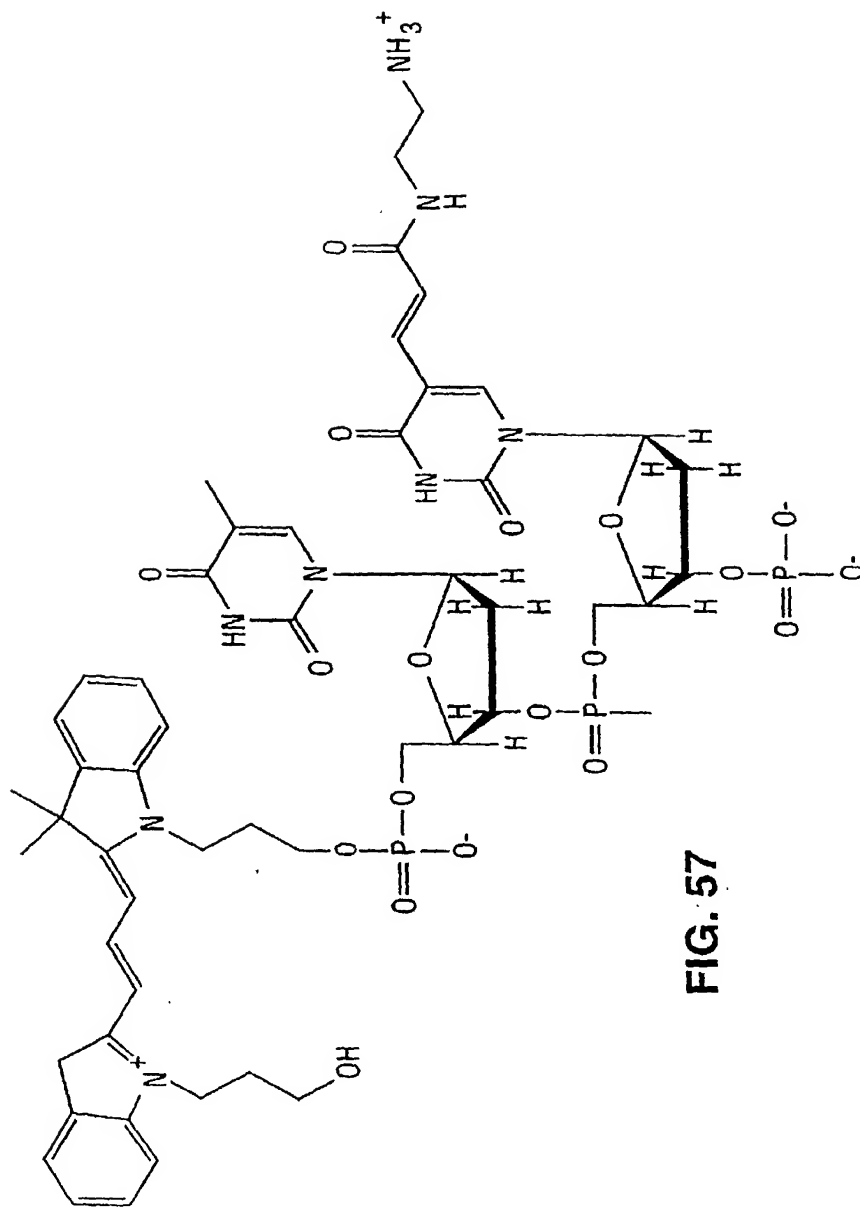
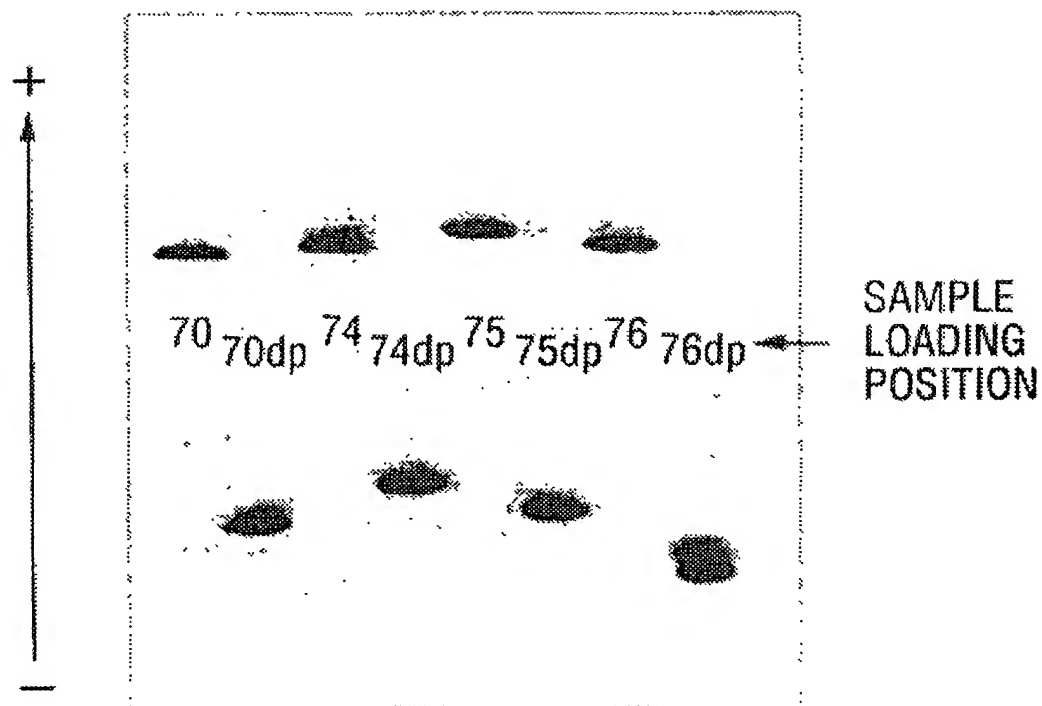


FIG. 57





**FIG. 58**

**FIG. 59**

$$\begin{array}{c}
 \text{NH}_3^+ \\
 | \\
 \text{5'---C}_y\text{'3---T---T---} \swarrow \text{Cleaveage Site} \\
 | \\
 \text{NH}_3^+
 \end{array}$$

INVADER  $\longrightarrow$  CTTTTCACCCAGCGAGACGGG-3' 61  
 M13  $\rightarrow$  3'CGCCAAACGCATAACCCGCGGTCCACCAAAAGAAAAGTGGTCTCTGCCC-5'  
 09876543210987654321  
 123456789  
 67  $\rightarrow$  ATTGGGCGCCAGGGTGGTTTTT

**FIG. 60A**

[illegible]

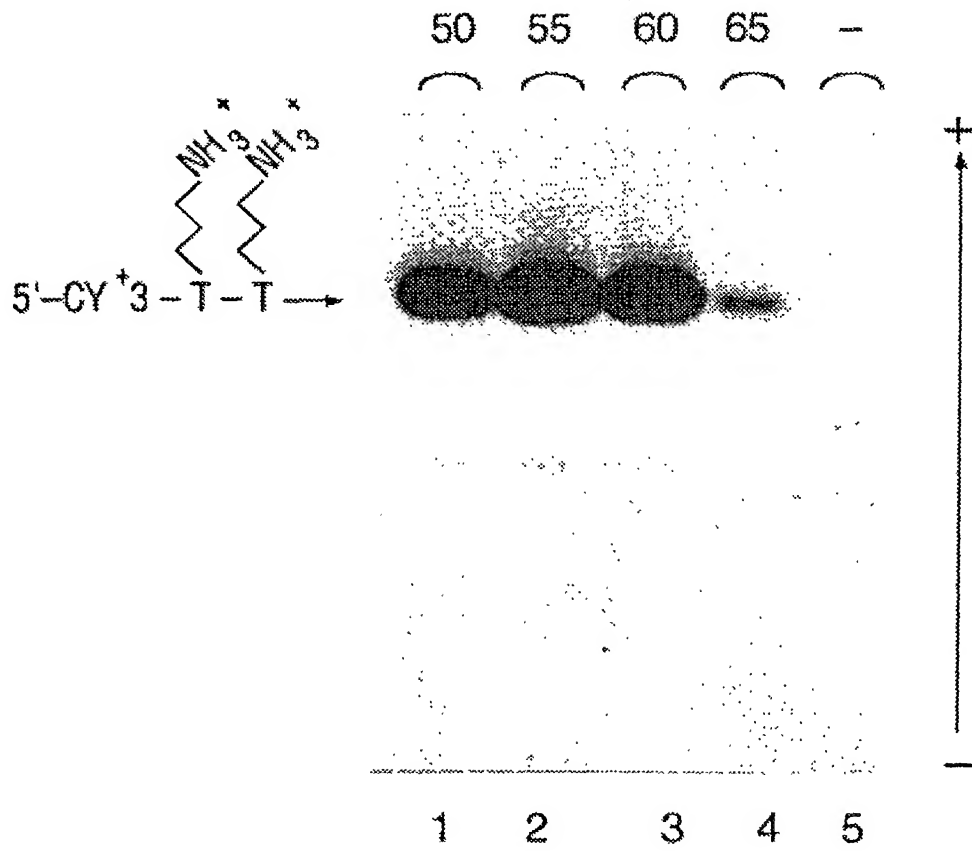


FIG. 60B

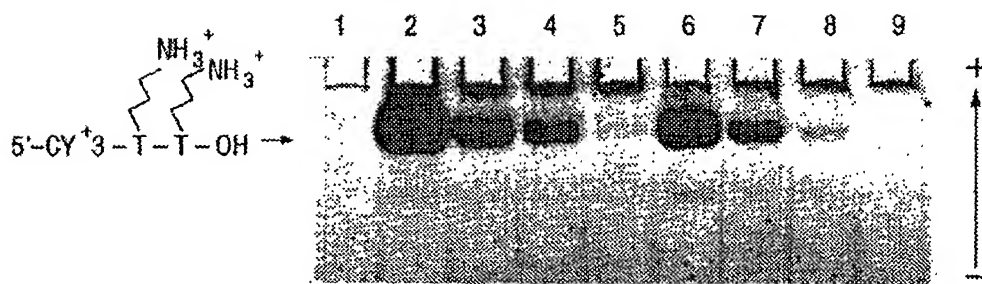


FIG. 61

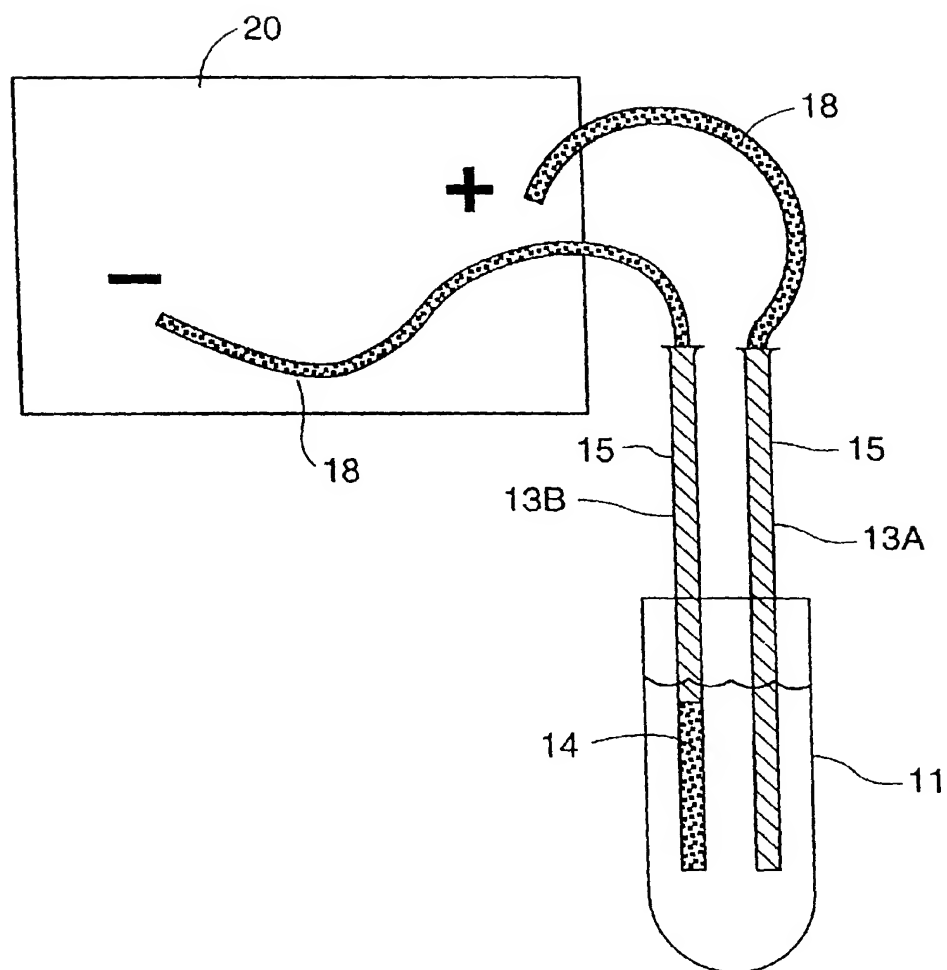


FIG. 62

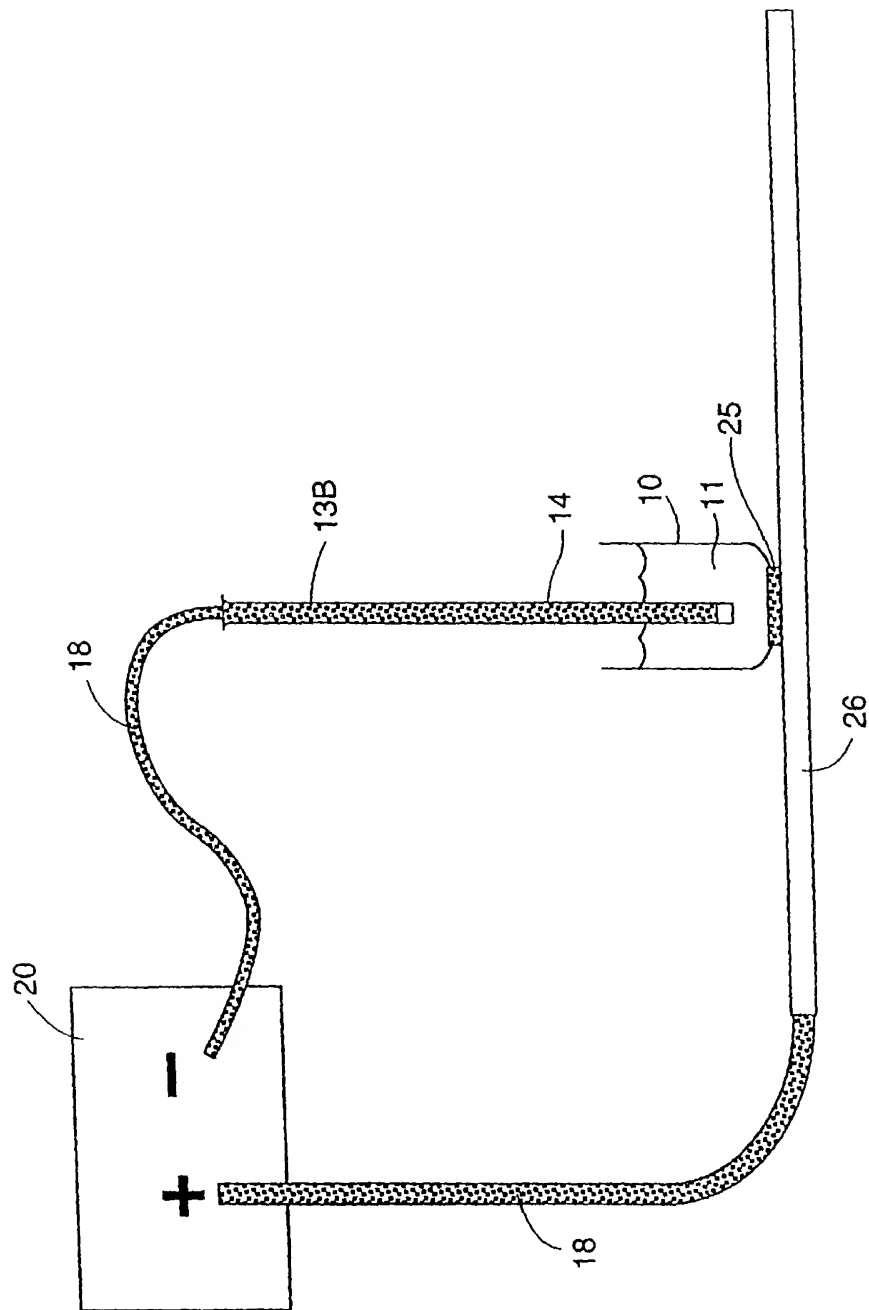


FIG. 63



FIG. 64





FIG. 65A



FIG. 65B



FIG. 65C



FIG. 65D

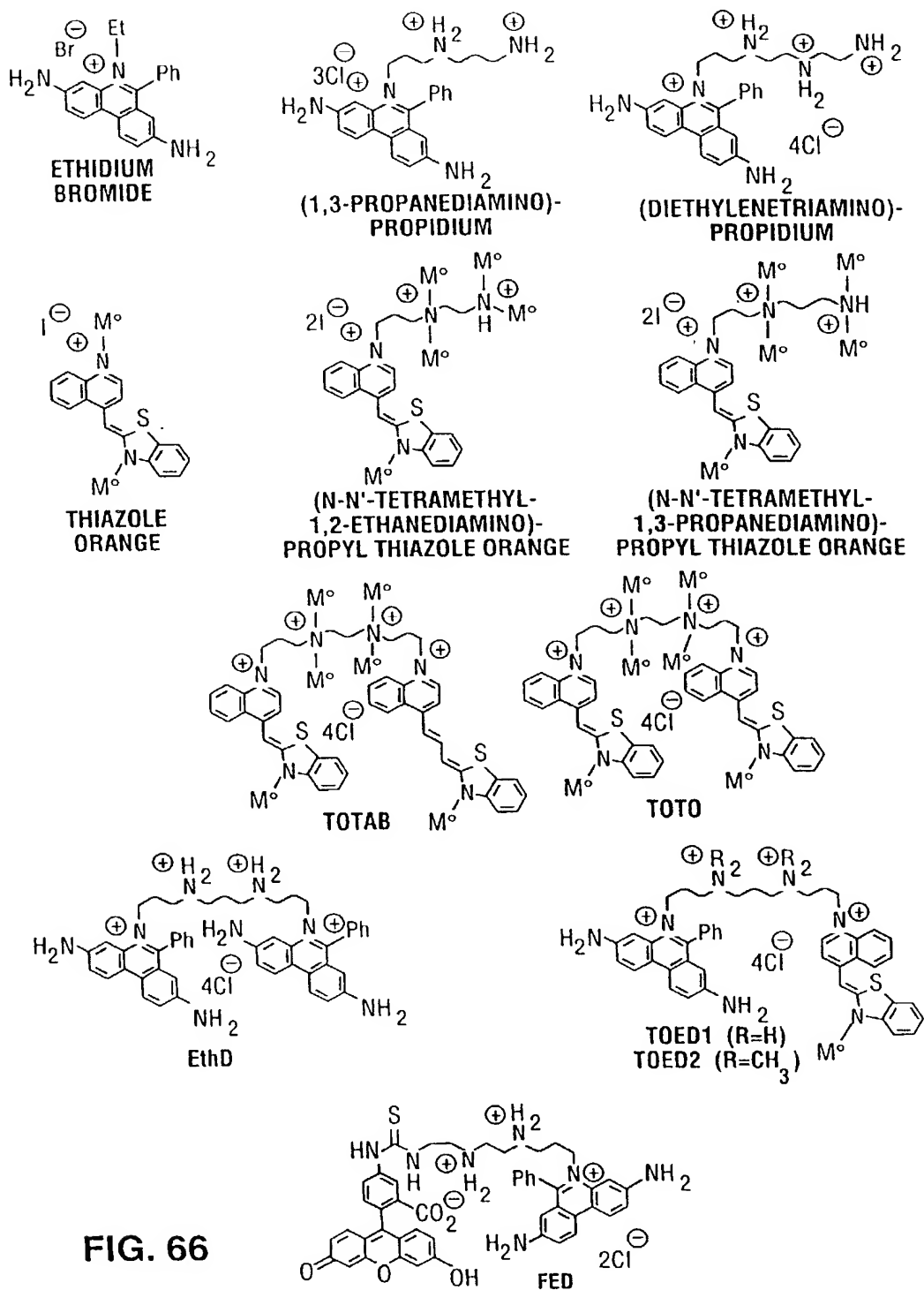


FIG. 66